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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                      Scoring table:
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PIR 79:*
1: pir1:*
2: pir2:*
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4: pir4:*
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150
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                                                                                                                                                                                                                                                                 283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                       QARQNLQNLFINFCLILICLLLICIIVMLL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                            7, 2005, 14:30:40 ; Search time 76 Seconds (without alignments)
37.980 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	43	410	ω <u>ω</u>	37	36	35	34	33	32	31	30
50	50	50	500	50	50	50	50	50	50	50	50
33.3	 			υ . ω . ω	33.3	33.3	33.3	33.3	33.3	33.3	33.3
488 511	484	389	388	359	348	226	226	226	226	226	226
N	2 -		N N	N	N	N	N	N	N	N	N
F86460	C88264	SAVLJ1	E72103	B59105	JC7907	JQ2059	JQ2062	JQ2057	JQ2060	JQ2061	JQ2058
protein-tyrosine k probable cytochrom	protein kin-15 [im		hypothetical prote	hypothetical prote	common cytokine re	surface antigen -					

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-52 <uy2> A;Residues: 1-52 <uy2> A;Cross-references: GB:M35393; NID:g164045; PIDN:AAC41618.1; PID:g164046 C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, ar C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplate; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation if C;Superfamily: cardiac phospholamban C;Superfamily: cardiac phospholamban C;Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr</uy2></uy2>	A;Molecule type: protein A;Residues: 1-35,'X',37-40,'X',42-45 <fuz> A;Residues: 1-35,'X',37-40,'X',42-45 <fuz> R;Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S. Nucleic Acids Symp. Ser. 17, 121-124, 1986 A;Title: Characterization of recombinant cDNA clones for canine cardiac phospholamban. A;Reference number: I46227; MUID:87174860; PMID:3562256 A;Accession: I46227; MUID:87174860; PMID:3562256</fuz></fuz>	A; Residues: 10-45 <sim's 10-45="" 1044-1050,="" 138,="" 1986="" <sim's="" a24818;="" a24818<="" a;="" a;title:="" accession:="" acetylation="" acid="" amino="" and="" biochem.="" biophys.="" by="" characterization="" commun.="" contents:="" f.="" fujii,="" h.;="" j.;="" kadoma,="" m.;="" muid:86323152;="" number:="" of="" partial="" phospholamban="" pmid:3753485="" r;="" reference="" res.="" residues:="" sakiyama,="" sequence="" sequencing="" site="" structural="" tada,="" td="" toda,="" unit=""><td>A; Molecule type: mRNA A; Residues: 1-52 < UYE> A; Residues: 1-52 < UYE> A; Cross-references: GB:Y00399; NID:g911; PIDN:CAA68461.1; PID:g912 A; Cross-references: GB:Y00399; NID:g911; PIDN:CAA68461.1; PID:g912 A; Cross-references: CB:Y00399; NID:g911; PIDN:CAA68461.1; PID:g912 A; Simmerman, H.K.B.; Collins, J.H.; Theibert, J.L.; Wegener, A.D.; Jones, L.R. J. Biol. Chem. 261, 1333-1341, 1986 A; Title: Sequence analysis of phospholamban. Identification of phosphorylation sites A; Reference number: A25307; MUID:87008549; PMID:3759968 A; Contents: partial sequence and phosphorylation sites A; Accession: A25307 A.Molecule type: Trype: Tr</td><td>A;Molecule type: mRNA A;Residues: 1-52 <fuj> A;Residues: 1-52 <fuj> A;Cross-references: UNIPROT:P61012; GB:M16012; NID:g164043; PIDN:AAA30884.1; PID:g164044 R;Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S. Nucleic Acids Res. 15, 6738, 1987 A;Title: The cDNA sequence of the major phospholamban mRNA in canine cardiac ventricular A;Reference number: A26805; MUID:87316936; PMID:3628007 A;Accession: A26805</fuj></fuj></td><td>RESULT 1 A29002 A29002 phospholamban - dog C;Species: Canis lupus familiaris (dog) C;Dace: 23-Aug-1987 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004 C;Dacesion: A29002; A26805; A25307; A24818; I46227 C;Accession: A29002; A26805, Tanaka, S.; Kadoma, M.; Tada, M. R;Fujii, J.; Ueno, A.; Kitano, K.; Tanaka, S.; Kadoma, M.; Tada, M. J. Clin. Invest. 79, 301-304, 1987 A;Title: Complete complementary DNA-derived amino acid sequence of canine cardiac phosp) A;Reference number: A29002; MUID:87083954; PMID:3793929</td><td>ALIGNMENTS</td></sim's>	A; Molecule type: mRNA A; Residues: 1-52 < UYE> A; Residues: 1-52 < UYE> A; Cross-references: GB:Y00399; NID:g911; PIDN:CAA68461.1; PID:g912 A; Cross-references: GB:Y00399; NID:g911; PIDN:CAA68461.1; PID:g912 A; Cross-references: CB:Y00399; NID:g911; PIDN:CAA68461.1; PID:g912 A; Simmerman, H.K.B.; Collins, J.H.; Theibert, J.L.; Wegener, A.D.; Jones, L.R. J. Biol. Chem. 261, 1333-1341, 1986 A; Title: Sequence analysis of phospholamban. Identification of phosphorylation sites A; Reference number: A25307; MUID:87008549; PMID:3759968 A; Contents: partial sequence and phosphorylation sites A; Accession: A25307 A.Molecule type: Trype: Tr	A;Molecule type: mRNA A;Residues: 1-52 <fuj> A;Residues: 1-52 <fuj> A;Cross-references: UNIPROT:P61012; GB:M16012; NID:g164043; PIDN:AAA30884.1; PID:g164044 R;Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S. Nucleic Acids Res. 15, 6738, 1987 A;Title: The cDNA sequence of the major phospholamban mRNA in canine cardiac ventricular A;Reference number: A26805; MUID:87316936; PMID:3628007 A;Accession: A26805</fuj></fuj>	RESULT 1 A29002 A29002 phospholamban - dog C;Species: Canis lupus familiaris (dog) C;Dace: 23-Aug-1987 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004 C;Dacesion: A29002; A26805; A25307; A24818; I46227 C;Accession: A29002; A26805, Tanaka, S.; Kadoma, M.; Tada, M. R;Fujii, J.; Ueno, A.; Kitano, K.; Tanaka, S.; Kadoma, M.; Tada, M. J. Clin. Invest. 79, 301-304, 1987 A;Title: Complete complementary DNA-derived amino acid sequence of canine cardiac phosp) A;Reference number: A29002; MUID:87083954; PMID:3793929	ALIGNMENTS

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C;Accession: A49057
R;Ganim, J.R.; Luo, W.; Ponniah, S.; Grupp, I.;
Circ. Res. 71, 1021-1030, 1992
A;Title: Mouse phospholamban gene expression du
A;Reference number: A49057; MUID:93008802; PMID
A;Accession: A49057
A;Molecule type: mRNA
A;Residues: 1-52 <GAN>
A;Cross-references: UNIPROT:P61014; GB:S46792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phospholamban - 1
C;Species: Oryctc
C;Date: 28-Feb-15
C;Accession: B404
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C;Species: Mus
C;Date: 19-Dec
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A;Experimental source: cardiac muscle
A;Note: sequence extracted from NCBI backbone (NCBIN:116999, NCBIP:117001)
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, are
C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplase; after phospholamban is the major phosphorylated and the rate of muscle relaxation in C;Superfamily: cardiac phospholamban
C;Superfamily: cardiac phospholamban
C;Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
F;31-52/Domain: transmembrane #status predicted <TMM'>
F;15/Modified site: acetylated amino end (Met) #status predicted
F;16/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predict
                                                                                                                                                                     A;Cross references: UNIPROT:P61015; GB:M63601; NID:g165636; R;Fujii, J.; Lytton, J.; Tada, M.; MacLennan, D.H. FBBS Lett. 227, 51-55, 1988
A;Title: Rabbit cardiac and slow-twitch muscle express the £A;Reference number: S00249; MUID:88112222; PMID:2962883
A;Accession: S00249
          C; Comment:
                                                                         A; Molecule type: mRNA
A; Residues: 1-52 < FU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Feb-1992 #sequence revision 27-Jun-1994
C;Accession: B40424; S00249
R;Fujii, J.; Zarain-Herzberg, A.; Willard, H.F.; Ta
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                                                                                                                                            A;Status: not compared with
                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-52 < FUJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A40424;
A;Accession: B40424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Pujii, J.; Zarain-Herzberg, A.; Willard, H.F.; Tada, M.; Ma
J. Biol. Chem. 266, 11669-11675, 1991
A;Title: Structure of the rabbit phospholamban gene, cloning
A;Reference number: A40424; MUID:91268032; PMID:1828805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B40424
                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: DNA
                                      Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Mus musculus (house mouse);Date: 19-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
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Best Local
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Best Local
          Phospholamban
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site: acetylated amino end (Met) #status experimental
site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status expersite: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status
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llarity 100.0%;
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                                      GB:Y00761; NID:g1661;
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          expressed
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Pred. No. 2.9e-11;
; Mismatches 0;
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          ä
          cardiac
PIDN:CAA68730.1; PIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 52;
       PID:g1662
low twitch
                                                                                                                                                                                                                                              same
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          skeletal
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cipate: 05-Mar-1994 #sequence_revision 27-Jun-1994 #text_Cipate: 05-Mar-1994 #sequence_revision 27-Jun-1994 #sequence_revision 27-J
       R;Johns, D.C.; Feldman, A.M.
Biochem. Biophys. Res. Commun. 188, 927-933, 1992
B;othem. Identification of a highly conserved region at A;Reference number: I52270; MUID:93075183; PMID:1445334
A;Accession: I52270
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                                                                                                                                                                            A; Cross-references: UNIPROT: P61016;
                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-52 < SHA>
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EMBL:X71068; NID:g313809;

PIDN: CAA50394.1;

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27-Jun-1994 #text_change

09-Jul-2004

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phospholamban - pig
C;Species: Sus scrofa
C;Date: 21-Nov-1993 †
C;Daccession: S05540
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A;Residues: 1-52 <VER.
A;Residues: 1-52 vER.
A;Residues: 1-52 vER.
A;Cross-references: UNIPROT:P61013; EMBL:X15075; NID:g2055; PIDN:CAA33171.1; PID:g2056
A;Cross-references: UNIPROT:P61013; EMBL:X15075; NID:g2055; PIDN:CAA33171.1; PID:g2056
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, and C;Comment: Phospholamban is the major phosphorylated anctivated and the rate of muscle sarcoplas, e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation in C;Superfamily: cardiac phospholamban
C;Superfamily: cardiac phospholamban
C;Keywords: acetylated amino end, AfPase inhibitor; muscle; pentamer; phosphoprotein; tr
F;31-52/Domain: transmembrane #status predicted <TMM>
F;1Modified site: acetylated amino end (Met) #status predicted
F;16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicts
F;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicts
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A;Note: only one gene was detected
A;Note: the single intron is upstream of the coding region
C;Superfamily: cardiac phospholamban
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C;Keywords: acetylated amino end; ATPase inhibitor;
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;11-52/Domain: transmembrane #status predicted /
;1/Modified site: acetylated amino end (Met) #status predicted /
;16/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status /
;17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #s
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;Date: 21-Nov-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
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Pred. No. 2.9e-11;
; Mismatches 0;
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A;Molecule type: mRNÀ
A;Residues: 1-52 cHPA2>
A;Cross-references: GB:895849; NID:9247934
A;Cross-references: GB:895849; NID:9247934
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, ar C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas Pase; after phosphorylation, the calcium pump is activated and the rate of muscle relaxs C;Superfamily: cardiac phospholamban
C;Keywords: acetylated amino end; ATPase inhibitor; cardiac muscle; heart; pentamer; pho F;31-52/Domain: transmembrane #status predicted <TMM>
F;31-52/Domain: transmembrane #status predicted <TMM>
F;31-52/Domain: transmembrane #status predicted <TMM>
F;31-52/Domain: transmembrane #status predicted <TMM-
F;31-52/Domain: transmembrane (Ser) (covalent) (by cAMP-dependent kinase) #status predicted site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status predicted site: phosphate (Thr) (cov
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A;Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, A;Reference number: A40424; MUID:91268032; PMID:1828805
A;Accession: A40424
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C;Superfamily: cardiac phospholamban
C;Keywords: accetylated amino end, ATPase inhibitor; muscle; pentamer; phosphoprotein;
C;Keywords: accetylated amino end, etc. actumer;
F;31-52/Domain: transmembrane #status predicted <TMM>
F;17Modified site: accetylated amino end (Met) #status predicted
F;16/Binding site: phosphare (Ser) (covalent) (by calmodulin-dependent kinase) #status predified site: phosphare (Thr) (covalent) (by calmodulin-dependent kinase) #status
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A;Cross-references: GDB:128300; OMIM:172405
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A;Residues: 1-52 <FUJ>
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Adv. Exp. Med. Biol. 304, 387-395, 1991
A;Title: Cloning phospholamban cDNA from rat aortic smooth
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A;Residues: 1-52 <HWAl>
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;Date: 28-Feb-1992 #sequence
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Pred. No. 2.9e-11;
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R;Bentley, D.
submitted to the EMBL Data Library, June 1994
                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F54E7.5 - Caenorha
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision
C;Accession: T34299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:M59038
C;Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, C;Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcopl e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation C;Genetics:
A;Note: only one gene was detected A;Note: the single intron is upstream of the coding region C;Superfamily: cardiac phospholamban C;Superfamily: cardiac phospholamban C;Keywords: acetylated amino end; AfPase inhibitor; muscle; pentamer; phosphoprotein; F;31-52/Domain: transmembrane #status predicted <TMM>
                                                                                                                     A;Residues: I-305 <BEN>
A;Cross-references: UNIPROT:Q20783; EMBL:U00067; PIDN:AAC77517.1; GSPDB:GN00021; CESP:F5
A;Experimental source: strain Bristol N2; clone F54E7
                                                                                                                                                                                                                                  A; Status: preliminary; translated
                                                                                                                                                                                                                                                           A;Reference number: Z21502
A;Accession: T34299
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A;Note: the sequence of residues
R;Toyofuku, T.; Zak, R.
                                                A; Introns: 78/3; 173/3
                                                                         A; Map position:
                                                                                               A;Gene: CESP:F54E7.5
                                                                                                                                                                                                            A; Molecule type: DNA
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F;1/Modified site: acetylated amino end (Met) #status predicted F;1/6/Binding site: phosphate (Ser) (covalent) (by cAWP-dependent F;16/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent)
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A;Molecule type: DNA
A;Residues: 1-52 <TO2>
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A; Title: Characterization of cDNA and genomic sequences
A; Reference number: A39535; MUID:91170195; PMID:1825996
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A; Residues: 1-52 < TO3 >
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A; Accession: A44531
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A; Residues: 1-17, 'L',
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C;Species: Gallus gallus (chicken)
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Pred. No. 9.
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probable O-antigen/teichoic acid transporter CAC3065 [imported] - Clostridium
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein cotel - human
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T08827
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A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: A81445
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A;Cross-references: UNIPROT:Q9PIM9; GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB727;
A;Experimental source: serotype O2, strain NCTC 11168
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A;Residues: 1-669 <WIN>
A;Cross-references: UNIPROT:P81408; EMBL:AF023268; NID:g2564910; PIDN:AAC51822.1;
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C;Superfamily: (
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Introns: 75/3; 94/3; 131/3; 171/3; 207/3; 266/2; 299/3; 323/1;
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Pred. No.
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Pred. No. 27;
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A,Cross-references UNIPROT:P39209; EMBL:Z34005; NID:g496483; PIDN:CAA83970.1; PID:g4964 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Erlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Lavita, K.; Lapidus, A.; Lardinois, M.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portectalle, M.; Gawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portectalle, Rieger, M.; Sachleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.; Person. Beorger, M. 196044033; PMID:9384377
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A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325, A;Accession: B97277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Microbiology 140, 1847-1854, 1994
A;Title: Identification of TlpC, a novel 62 kDa MCP-like
A;Reference number: 140495; MUID:95005439; PMID:7921238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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A;Cross-references: UNIPROT:Q97EP3; GB:AE001437; PIDN:AAK81005.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                              C; Superfamily: methyl-accepting chemotaxis protein
                                                                                                                                                                                                                          A;Residues: 1-215,'T',217-331,'P',333-573 <KUN>A;Cross-references: GB:Z99105; GB:AL009126; NID
                                                                                                                                                                                                                                                                                                                 A; Status: nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-573 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Hanlon, D.W.; Rosario, M.M.; Ordal, G.W.; Venema, G.; Van Sinderen, Microbiology 140, 1847-1854, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Bacillus subtilis
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I44496; B69724; S45067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methylation enzyme tlpC - Bacillus subtilis N; Alternate names: 62K MCP-like protein TlpC; methyl-accepting chemotaxis protein tlpC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              á
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CAC3065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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                                                                                                                                                                                                     A; Experimental source:
                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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Similarity 7; Conserv
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                       35.3%;
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Score 53; DB Pred. No. 42; 12; Mismatches
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Pred. No. 34;
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nonstructural protein 5B - human coronavirus (strain 229E)
C;Species: human coronavirus
C;Species: human coronavirus
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: C34038
R;Raabe, T.; Siddell, S.
Nucleic Acids Res. 17, 6387, 1989
A;Title: Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA 5 unique
A;Reference number: A34038; MUID:89366667; PMID:2701946
A;Accession: C34038
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MNIHH3
                                                                                    A;Molecule type: mRNA
A;Residues: 1-77 <JOU>
A;Cross-references: EMBL:X64942; NID:g59462; PIDN:CAA46114.1; PID:g59464
C;Superfamily: coronavirus nonstructural protein 5B
                                                                                                                                                                                                 A;Title: Sequence analysis of human coronavirus 229E mRNAs 4 and 5: evidence for polymor A;Reference number: S25708; MUID:92230395; PMID:1373555
A;Accession: S25709
A;Status: preliminary
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A; Residues: 1-77 < RAA>
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A;Molecule type: mRNA
A;Residues: 1-1880 <HUA>
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R;Huang, Y; Jellies, J.; Johansen, K.M.; Johansen, J.
R;Huang, Y, Jellies, J.; Johansen, K.M.; Johansen, J.
R;Huang, Y.; Jellies, J.; Johansen, J.
J. Cell Biol. 138, 143-157, 1997
A;Title: Differential glycosylation of Tractin and LeechCAM, two novel Ig-superfamily A;Reference number: Z18951; MUID:97362067; PMID:9214388
A;Accession: T18531
                                                                                                                                                                                                                                                                                                        R;Jouvenne, P.; Mounir, S.; Stewart, J.N.; Richardson, C.D.; Talbot, P.J. Virus Res. 22, 125-141, 1992
                                                                                                                                                                                                                                                                                                                                                  C;Accession: $25709
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;Keywords: nonstructural protein
Query Match 35.0%;
Best Local Similarity 40.0%;
Matches 10; Conservative
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; Score 52.5; D
; Pred. No. 11;
8; Mismatches
                                            DB 2;
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                                               Length 77;
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Qy 9 LFIN---FCLILICLLLICIIVMLL 30
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Search completed: July 7, 2005, 15:42:30 Job time: 77 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession accession number.
- accession number can be found by searching the old accession number in the UniProt Protein extension .rup) that can no longer be found in the database, the permanent record with the new If you encounter an accession number from an older search run against UniProt (results file Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

numbers members of the public who may encounter UniProt temporary accession include a copy of this attachment to assist any future Examiners or When submitting sequence search results for scanning into IFW, please Tnis Page Blank (uspto)

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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P61013 sus scrofa
P61015 oryctolagus
P61016 rattus norv
P26678 homo sapien
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Q80iw9
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6 rattus norv
8 homo sapien
7 gallus gall
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SEQUENCE FROM N.A. TISSUE-Heart ventricle; MEDLINE-87316936; PubMed-3628007; Wyeda A., Kitano K., Fujii J., Kadoma M., Tada M., Tanaka S.; Wyeda A., Kitano K., Fujii J., Kadoma M., Tada M., Tanaka S.; Wyeda A., Kitano K., Fujii J., Kadoma M., Tada M., Tanaka S.; Wyeda A., Kitano K., Fujii J., Kadoma M., Tada M., Tada M., Tanaka S.; Mucleic Acids Res. 15:6738-6738(1987). [3] SEQUENCE OF 1-45, AND ACETYLATION. MEDLINE-86323152; PubMed-3753485; Pujii J., Kadoma M., Tada M., Toda H., Sakiyama F.; Pujii J., Kadoma M., Tada M., Toda H., Sakiyama F.; Pujii J., Kadoma M., Tada M., Toda H., Sakiyama F.; Pujii J., Kadoma M., Tada M., Toda H., Sakiyama F.; Pujii J., Kadoma M., Tada M., Toda H., Sakiyama F.; Pujii J., Kadoma M., Tada M., Toda H., Sakiyama F.; Plostine Biophys. Res. Commun. 138:1044-1050(1986). SEQUENCE OF 10-45, AND PHOSPHORYLATION SITES SER-16 AND THR-17. MEDLINE-87008549; PubMed-3759968; Simmerman H.K.B., Collins J.H., Theibert J.L., Wegener A.D., Jones L.R.; PHOSPHORYLATION SITES SER-16 AND THR-17. MEDLINE-89291905; PubMed-2544595; Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; PHOSPHORYLATION SITES SER-16 AND THR-17. MEDLINE-89291905; PubMed-2544595; Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; PHOSPHORYLATION SITES SER-16 AND THR-17. MEDLINE-89291905; PubMed-2544595; Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; PHOSPHORYLATION SITES SER-16 AND THR-17. MEDLINE-89291905; PubMed-2544595; Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; PHOSPHORYLATION SITES SER-16 AND THR-17. MEDLINE-8921905; PubMed-2544595; Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; PHOSPHORYLATION SITES SER-16 AND THR-17. MEDLINE-8921905; PubMed-2544595; Wegener A.D., Simmerman H.K.B., Lindemann J.P., Jones L.R.; "The Serial	LT 1 CANFA CANFA CANFA CANFA CANFA CANFA CANFA CANFA COL - APR - 11 CAT CANFA CAT CANFA CAT CANFA CAN

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Cardiac phospholamban (
          SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Aorta, Heart, and Kidney;

MEDLINE=2235468; PubMed=12466851; DOI=10.1038/nature01266;

Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

Okazaki Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saito R., Nogami A., Schombach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

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Baldarelli R., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
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Ganim J.R., Luo W., Ponniah S., Grupp I., Kim H.W., Ferguson D.G.,
Kadambi V., Neumann J.C., Doetschman T., Kranias E.G.;
"Mouse phospholamban gene expression during development in vivo and
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Grimmond S., Gu
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INTERPROSE PLB; 1.
PIRSPOOL665; PLB; 1.
TIGREAMS; TIGR01294; P lamban; 1.
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Phosphothreonine (by CaMK1).
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EMBL; AK052199; BAC34880.1; --
EMBL; BC061097; AAH61097.1; --
                  InterPro; IPR005984; Plamban.
PIRSF; PLB; 1.
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RX MEDLINE-22388.57; PubMed=12477932; DOI=10.1073/pnas.242603899;
RRA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RRA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RRA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RRA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RRA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RRA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RRA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RRA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
RRA Richards S., Worley K.C., Young A. C., Shevchenko Y., Bouffard G.G.,
RRA Rodrigues A.C., Grimwood J., Schmutz J., Myers R.M.,
RRA Generation and initial analysis of more than 15,000 full-length human
RT and moule collaboration and initial analysis of more than 15,000 full-length human
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RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Maglott D.R., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang I.,
RA Wilming L.G., Wynshaw-Boris A., Yangaisawa M., Yang I., Yang I.,
RA Wilming L.G., Wynshaw-Boris A., Zimmer A., Carninci P., Hayatsu N.,
RA Wilming L.G., Wynshaw-Boris A., Yangaisawa M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aliawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
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"Analysis of the mouse transcriptome based on functional annotation of
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entities requires a license
                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Belongs to the phospholamban family.
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s requires a license agreement (S an email to license@isb-sib.ch).
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                                                        (See http://www.isb-sib
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01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Cardiac phospholamban (PLB).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a licement greement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "NMR solution structure of phospholamban membrane Submitted (AUG-2000) to the PDB data bank.
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"cDNA cloning and sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE ....
SEQUENCE ....
ISSUE-Smooth muscle;
MEDLINE-90056437; PubMed-2530978;
MEDLINE-90056437; PubMed-2530978;
MUYTACK F., Eggermont J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=Smooth musc
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Vorherr T., Krebs J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitted (AUG-2000) to the PDB data bank.

PUNCTION: Phospholamban has been postulated to regula activity of the calcium pump of cardiac sarcoplasmic SUBUNIT: Homopentamer (By similarity).

SUBCELLULAR LOCATION: Membrane (By similarity).
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                 N-acetylmethionine (By similarity).
Phosphoserine (by PKA) (By similarity).
Phosphothreonine (by CaMK1) (By
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y PKA) (By similar
(by CaMK) (By
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RESULT 4
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P61015; P200
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EMBL; M63601; AAA31445.1; -.
EMBL; Y00761; CAA66730.1; -.
PIR; B40424; B40424.
                                                                     IntAct; P61015; -.
InterPro; IPR005984; P lamban.
PIRSF; PIRSF001655; PLB; 1.
TIGRPAMs; TIGR01294; P lamban;
Acetylation; PhosphoryTation; 7
                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=91268032; PubMed=1828805;

MIDITUS J. Zarain-Herzberg A., Willard H.F.,

Fujii J., Zarain-Herzberg Phospholamban gene

"Structure of the rabbit phospholamban gene

CDNA, and assignment of the gene to human cl

J. Biol. Chem. 266:11669-11675(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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01-FEB-1991 (Rel. 17, Last seq
25-OCT-2004 (Rel. 45, Last ann
                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                      between
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"Rabbit cardiac a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=PLN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cardiac phospholamban
                                                                                                                                  HSSP; P07473; 1FJK.
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88112222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                      PTM: Phosphorylated in response to beta-adreners SIMILARITY: Belongs to the phospholamban family.
                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Membrane. TISSUE SPECIFICITY: Heart.
                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homopentamer.
                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Phospholamban activity of the calcium
                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EW
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                                                                                                                                                                                                                                                                                                                                                                                                                    2; PubMed=2962883; DOI=10.1016/0014-5793(88)81412-1;
n J., Tada M., Maclennan D.H.;
and slow-twitch muscle express the same phospholamb
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           N-acetylmethionine (By similarity) Phosphoserine (by PKA) (By similar Phosphothreonine (by CaMK) (By
                                               Cytoplasmic Potential.
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                                                       Transmembrane.
Cytoplasmic (Potential).
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Pred. No. 1.2e-10;
; Mismatches 0;
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RESULT 5
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                                                                                                                                        EMBL; L03382; AAA41849.1; -.
EMBL; X71068; CAA50394.1; -.
EMBL; S95849; AAN86727.1; -.
EMBL; S95853; AAB21903.1; -.
PIR; S37638; S37638.
HSSP; P07473; 1FJK.
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                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shanahan C.M., Weissberg P.L., Metcalfe J.C.; "Isolation of gene markers of differentiated and proliferating vascular smooth muscle cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92206263; PubMed=1725098; Hwang K.S., Nadal-Ginard B.;
InterPro; IPRO05984; Plamban.
PIRSF; PIRSF001665; PLB; 1.
TIGRPAMs; TIGR01294; Plamban; 1.
Acetylation; Phosphorylation; Transmembrane DOMAIN
1 31 Cytoplasmic (Pd. Cytoplasmic 
                                                                                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93284726; PubMed=8508530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phospholamban gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johns D.C., Feldman A.M.; "Identification of a highly conserved region at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93075183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity of the calcium pump of cardiac s
SUBUNIT: Homopentamer.
SUBCELLULAR LOCATION: Membrane.
TISSUE SPECIFICITY: Heart.
PTM: Phosphorylated in response to beta-a
SIMILARITY: Belongs to the phospholamban
                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
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Pred. No. 1.2e-10;
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                                                                                                                                                                          WEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Altschni S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschni S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschni S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschni S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschni S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Altschnko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Altschnko L., Marusina K., Farmer A.A., Rubin G.M., Prange C.J.,

X Altschnko L., Warley N.B., Foshiyuki S., Carninci P., Prange C.J.,

X Altschni S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullahy S.J.,

X Altschn D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Altschn D.K., Marus D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Altschn D.K., Touchman M., Madan A., Rodrigues S., Sanchez A.,

X Hilland A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Holting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Holting A.C., Grimwood J., Schmutz J., Myers R.M.,

X Butterfield Y.S.N., Krzywinski M.J., Marya M.A.,

X Chang A. C., Schein J. F., Tones S. J. M. Marya M.A.,

X Chang A. C., Schein J. F., Tones S. J. M. Marya M.A.,

X Chang A. C., Schein J. F., Tones S. J. M. Marya M.A.,

X Chang A. C., Schein J. F., Tones S. J. M. Marya M.A.,

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X Chang A. C., Schein J. F., Tones S. J. M. Marya M.A.,

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X Chang A. C., Schein J. F., Tones S. J. M. Marya M.A.,

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99222499; PubMed=10198197; DOI=10.1006/jmcc.1998.0904; McTiernan C.F., Frye C.S., Lemster B.H., Kinder E.A., Ogletree-Hughes M.L., Moravec C.S., Feldman A.M.; "The human phospholamban gene: structure and expression."; J. Mol. Cell. Cardiol. 31:679-692(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning of human cardiac phospholamban."; Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salvatore C.A., Jacobson M.A.; "Cloning of human cardiac phos
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01-AUG-1992 (Rel.
25-OCT-2004 (Rel.
                                                                                                                     Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cardiac
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0763601F76A854D3 CRC64;
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Pred. No. 1.2e-10;
                                                                 99:16899-16903 (2002)
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Mullahy S.J.,
Tathe P.H.,
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MEDLINE=95298769; PubMed=7779806;

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Query Match
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Matches 29; Conser
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EMBL; M60411; AAA60109.1; -.
EMBL; M60411; AAD55595.1; -.
EMBL; BC005269; AAH05269.1; -.
EMBL; BC005269; AAH05269.1; -.
PIR; A40424; A40424.
PDB; 1K9N; Model; A/B/C/D/E=35-52.
PDB; 1K9N; Model; A/B/C/D/E=35-52.
PDB; 1FLN; Model; A/B/C/D/E=35-52.
PDB; 1PLN; Model; A/B/C/D/E=1-52.
PDB; 1PLP; NMR; @=1-25.
PDB; 1PLP; MOdel; A/B/C/D/E=1-52.
Genew; HONC:9080; PLN.
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PIRSF; PIRSF001665; PLB; 1.
TIGRPAMB; TIGR01294; Plamban; 1.
3D-structure; Acetylation; Phosphor DOMAIN
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MOD_RES 17 17 Phosph
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"Using experimental information to produce a model of the
transmembrane domain of the ion channel phospholamban.";
Biophys. J. 74:1203-1214(1998).

-i- FUNCTION: Phospholamban has been postulated to regulate the
activity of the calcium pump of cardiac sarcoplasmic reticul
-i- SUBUNIT: Homopentamer.
-i- SUBCELLULAR LOCATION: Membrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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Adams P.D., Arkin I.T., Engelman D.M., Bruenger A.T.;
"Computational searching and mutagenesis suggest a st
pentameric transmembrane domain of phospholamban.";
Nat. Struct. Biol. 2:154-162(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: Phosphorylated in response to beta-adrenergic stimulation SIMILARITY: Belongs to the phospholamban family.
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                                                                                                                                                                                   MW.
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Pred. No. 6.3e
0; Mismatches
                                                                                                                                                                                                                                                                   N-acetylmethionine (By similarity).
Phosphoserine (by PKA) (By similarity).
Phosphothreonine (by CaMK) (By similarity).
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                                                                                                            144; DB 1;
No. 6.3e-10;
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                                                                                                                                      Length 52;
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PPLA_CHICK
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EMBL; M59037; -; NOT ANNOTATED CDS
EMBL; M59038; AAA63167.1; -.
PIR; A39535; A39535.
PIR; P07473; 1FJK.
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                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                               InterPro; IPR005984; P lamban.
Pfam; PF04272; Phospholamban; 1.
PIRSF; PIRSF001665; PLB; 1.
TIGRFAMs; TIGR01294; P lamban; 1.
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-!- SUBCELLULAR LOCATION: Membrane.
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01-AUG-1992 (Rel. 23, Last sequence up
25-0CT-2004 (Rel. 45, Last annotation

    -1- FUNCTION: Phospholamban has been postulated
activity of the calcium pump of cardiac sarc

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MEDLINE=91170195; PubMed=1825996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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Pred. No. 4.3e-09;
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Q20783;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein F54E7.5,
Name=F54E7.5; ORFNames=F54E7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
Eukaryota; Alveolata;
SEQUENCE FROM I
STRAIN-Bristol
                                                                                                           Waterston
Submitted
                                                                                                                                                                                                                                                                                                 "The sequence of C. Submitted (OCT-1994
                                                                                                                                                                                                                                                                                                                                                                          Bentley D.;
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2;
MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
SEQUENCE 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
                                                                                                                                                                             STRAIN-Bristol N2;
                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WormBase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _TaxID=6239;
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12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HMQNLF-NYIFYFVCLLLVIQIVLIL
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                                                                                                               (NOV-2002)
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792 AA;
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                                      N.A
                                                                                                                                                                                                                           N.A.
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4) to the
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46.2%;
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EMBL/GenBank/DDBJ databases.
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                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59.5;
Pred. No. 5:
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Moule S., Murphy L.,
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R., Corton C.,
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lin N., Hance Z.,
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                                                                                                                                                                                                                                                                                                                                                                                                                              RC STRAIN-ECS7BL/GJ; TISSUE-Stomach, and Tongue;
RC MEDLINE-22354683; PubMed=1246685; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nadarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schrimf L.M., Kamapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Schrimf L.M., Kamapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Gassterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzlerski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzlerski R.M., King B.L.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Magashhan T., Numata K., Okido T., Pavan M.J., Pertea G., Pesole G.,
RA Nagashima T., Numata K., Okido T., Pavan M.J., Pertea G., Pesole G.,
RA Nagashima T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sahtana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vasai T., Reed J.C., Wang Y., Watanabe Y., Wells C.,
Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
Walla C., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Sato K.,
Sato
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Matches
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TISSUE=Manmary gland;
TISSUE=Manmary gland;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R. E., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler '
Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.
Hopkins R.F., Jordan H., Moore T., Max S.L., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003
28-FEB-2003
05-JUL-2004
Sarcolipin.
                                                                                                                                                                                                                          Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Bairney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotati 60,770 full-length cDNAs";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
SARL N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WormBase; WBGene00018828; F54E7. WormBep; F54E7.5; CE01316. Hypothetical protein. SEQUENCE 305 AA; 34300 MW; (
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(Rel.
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41,
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54.2%;
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Last annotation updat
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Pred. No. 3
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RESULT 11
Q6SLE7
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Best Local S
Matches 11
Hori H., Ishikawa I.,
Submitted (NOV-2003) to the EMBL/Gense
SMBL; AY456000; AAR19044.1; -.
EMBL; AY456000; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0030234; F:enzyme regulator ac
R InterPro; IPR008028; Sarcolipin.
R Pfam; PF09366; Sarcolipin; 1.
R Pfam; PF09366; Sarcolipin; 1.
                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                  STRAIN=Wistar; TISSUE=Atrium; Minamisawa S., Yokoyama U., S. Hori H., Ishikawa Y.;
                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                        Q6SLE7;
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                       Q6SLE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AKO08863; -, NOT ANNOTATED_CDS.
EMBL; AKO08896; BAB25959.1; -
EMBL; AKO09005; BAB26019.1; -
EMBL; AKO09809; BAB26516.1; -
EMBL; AKO09809; BAB26516.1; -
EMBL; BCO28496; AAH28496.1; -
HSSP; O00631; 1JDM
MGD; MGI:1913652; Sln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaln D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Helton E., Ketteman M., Madan A., Garigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length humar
                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse cDNA sequences.";

C. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

SUBUNIT: Associated with calcium ATPase SERCAL.

SUBCELLULAR LOCATION: Membrane-associated. Sarcoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF05366; Sarcolipin;
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                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reticulum; Transmembrane
8 25 Potentia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3808 MW;
                                                                                                                                                                                                            Chordata;
Rodentia;
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Last annotation update)
                                                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                  Sato Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 6.3;
8; Mismatches
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Pred. No.
           9B310161575EF81D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential
                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                      activity;
                                                                                                                                 Nakagome
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                                                                                                                                                                                                            Murinae; Rattus
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RESULT 12
Q70V94
ID Q70V99
AC Q70V9
AC Q70V9
DT 05-JU
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Best Local S
Matches 16
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Best Local S
Matches 11
                                                                                                                                                                                                                           Q9PIM9 PRELIMINARY; PRT; 1
Q9PIM9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seque:
01-MAR-2004 (TrEMBLrel. 26, Last annot.
Putative integral membrane protein.
OrderedLocusNames=Cj0266.3, Cj0266c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Syst. Entomol. 29:371-382(2004).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAI
-!- SIMILARITY: Belongs to the complex I subuni
EMBL; AU353566 CAD59806.1; -
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0005739; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001694; Resp NADH_dhl.
Pfam; PF00146; NADHdh; 1.
                                                                                                                            Campylobacteria; Epsilonproteobacteria; Campylobacterales;
NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Preliminary evolutionary relationships genus Cotesia (Hymenoptera: Braconidae: analysis of four molecular markers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q70V94
Q70V94;
Q5-JUL-2004 (TrEMBLrel. 27,
Q5-JUL-2004 (TrEMBLrel. 27,
Q5-JUL-2004 (TrEMBLrel. 27,
MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088; Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churc Basham D., Chillingworth T., Davies R.M., Feltwell T., H
                                                                         STRAIN=NCTC 11168;
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone
NON_TER 1 1
NON_TER 130 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=217438;
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130 AA;
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ilarity 53.3%;
Conservative
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Liel. 27, Last annotation update)
subunit 1 (Fragment).
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45.8%;
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Last annotation update)
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Pred. No. 22;
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subunit 1
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T., Holro
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       Holroyd
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S. T.
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Q8BS41
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Best Local
                                 Q8BS41 PRELIMINARY; PRT;
Q8BS41;
Q8BS41;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence of the sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6V2B7 PRELIMINARY; PRT; 35 AA.
Q6V2B7;
Q5-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 1 (Fragment).
Bidessodes limestonensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL139074; CAB72734.1; -.
PIR; A81445; A81445.
InterPro; IPR010916; TONB Box N.
PROSITE; PS00430; TONB_DEFENDENT_REC_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reveals hypervariable sequences.";
Nature 403:665-668(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00146; NADHdh; Mitochondrion; NAD; Ox:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=14761060;
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Neoptera; Endopterygota; Coleoptera; Adephaga; Dytiscidae;
Hydroporinae; Bidessini; Bidessodes.
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"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quail M.A.,
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23, Last sequence update)
25, Last sequence update)
25, Last annotation update)
3 aorta and vein cDNA, RIKEN full-length
3:A530008A08 product:hypothetical protein
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tles (Coleoptera:
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Matches
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RE SEQUENCE FROM N.A.

RE STRAIN-C57BL/61; TISSUE-AORTA and vein;

RE STRAIN-C57BL/61; TISSUE-AORTA and vein;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiraoko K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saltoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hasuura S., Kawai J., Watanitaki Y., Muramatsu R., Kawai J., Sakayashizaki Y., Muramatsu S., Kawai J., Sakayashizaki Y., Muramatsu S., Kawai J., Sakayashizaki Y., Muramatsu S., Kawai J., Sakayashizaki Y., Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/60; TISSUE=Aorta and vein;
MEDLINE=2049374; PubMed=11042159; DDI-10.1101/gr.145100;
MEDLINE=2049374; PubMed=11042159; DDI-10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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STRAIN=C57BL/6J; TISSUE=Aorta and vein;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
[1]
                                                                                                                                     Hypothetical protein. SEQUENCE 110 AA; 1
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                                                                                                                                                                                                        EMBL; AK040657; BAC30658.1;
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qabe Y., Tagami M
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US-09-722-440-5
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e 5, Appli
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e 17, Appli
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33.3	33.3	33.3	33.3	33.7	34.0	34.0	34.0	34.0	34.0	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7
154	154	154	154	218	584	149	149	114	114	1203	1203	1203	1203	1182	1182	713	529
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
16, Appl	15, Appl	14, Appl	13, Appl	4489, Ap	22, Appl	48513, A	33296, A	55014, A	39797, A	2, Appli	2, Appli	2, Appli	2, Appli	7, Appli	7, Appli	4559, Ap	2, Appli

ALIGNMENTS

RESULT 1 US-09-252-063-3

GENERAL INFORMATION:

Sequence 3, Application US/09252063 Patent No. 6538022

APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Tenhunen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Yliperttula-Ikonen, M
APPLICANT: Tilgmann, Carola

Marjo

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Sequence 4, Application US/09252063
Patent No. 6538022
GENERAL INFORMATION:
APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Vadgren, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Lotta, Timo
APPLICANT: Kaivola, Juha
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; LENGTH: 52
; TYPE: PRT
; ORGANISM: Canis s
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Matches
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APPLICANT: Kaivola, Juha
APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER APPLING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTMARE: Patentin Ver. 2.0
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APPLICANT: Collegello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Ovaska, Martti
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vilgrenttula-Ikonen, Marjo
APPLICANT: Tilgmann, Carola
APPLICANT: Tilgmann, Carola
APPLICANT: Lotta, Timo
APPLICANT: Kaivola, Juha
ITITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
ITITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
ITITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
ITITLE OF INVENTION: Co-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER OF ESG ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
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US-09-252-063-5
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LENGTH: 52
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                    Sequence 6, Application US/09252063 Patent No. 6538022
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APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Tenhunen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vilperttula-Ikonen, Marjo
APPLICANT: Tilgmann, Carola
APPLICANT: Lotta, Timo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on TITLE OF INVENTION: Ca-ATPASE (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 4.4e-13;
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Pred. No. 4.4e-13;
; Mismatches 0;
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                     APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Broenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (GRV/RE)
CURRENT APPLICATION UNMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
    PRIOR APPLICATION NUMBER: GB 9908670.4
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RESULT 5
US-09-549-872B-14
                                      US-09-549-872B-15
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APPLICANT: Groenen, Jose
APPLICANT: Bogeart, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 998670.4
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
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; ORGANISM: Mus
US-09-252-063-6
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NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 6
LENGTH: 52
Sequence 15, Application US/09549872B Patent No. 6540996
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SEQ ID NO 14
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TITLE OF INVENTION: Compounds for Deactiv:
TITLE OF INVENTION: Co-ATPase (Phospholam)
FILE REFERENCE: 1102.0250001
FULL REFERENCE: 1102.0250001
FULL REFERENCE: 1102.0250001
FULL REFERENCE: 1102.0250001
FULL REFERENCE: 109/09/252,063
CURRENT FILING DATE: 199-02-18
EARLIER APPLICATION NUMBER: 08/937,117
                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Sus
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llarity 100.0%;
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Pred. No. 4.4e-13;
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Pred. No. 4.4e-13;
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PRIOR APPLICATION NUMBER: 09/252,063
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
EQ ID NO 3
ENGSTH: 52
TYPE TO STAN THE SEC ID NOS: 10
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SEQ ID NO 15
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
US-09-549-872B-15
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                                                                                                                                                                                                              Sequence 4, Application US/09722440 Patent No. 6774103
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
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                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                      APPLICANT: Pollegello, Piero APPLICANT: Ovaska, Martti APPLICANT: Tenhunen, Jukka APPLICANT: Vidgren, Jukka APPLICANT: Yliperttula-Ikone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Vidgren, Junne
APPLICANT: Yliperttula-Ikonen, Marjo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lotta, Timo
APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function
TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/722,440
CURRENT FILING DATE: 2000-11-28
                                                                         APPLICANT:
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                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-04-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Canis sp.
CANT: Lotta, Timo
CANT: Kaivola, Juha
CP INVENTION: Compounds for Deactivating Phospholamban Function on
                                                                                                                                                                                                                                                                                                                                 23 QARQNLQNLFINFCLILICLLLICIIVMLL 52
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Vidgren, Jukka
                                                                                          Yliperttula-Ikonen,
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                                                                         Tilgmann,
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                         Carola
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                                                                                            Marjo
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RESULT 10 US-09-722-440-6

Sequence 6, Application US/09722440 Patent No. 6774103 GENERAL INFORMATION:

APPLICANT: Pollesello, Piero APPLICANT: Ovaska, Martti

APPLICANT: APPLICANT:

Tenhunen, Jukka Vidgren, Jukka Vliperttula-Ikonen, Marjo Vligmann, Carola Lotta, Timo

APPLICANT:

Kaivola, Juha

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                                                                                                                                                                    SEQ ID NO 5
LENGTH: 52
TYPE: PRT
ORGANISM: Rattus sp.
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Tenhunen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vilgerttula-Ikonen, Marticant APPLICANT: Tilgmann, Carola
APPLICANT: Lotta, Timo
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                                                                            Matches
                                                                                             Best Local
                                                                                                                 Query Match
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APPLICANT: Kaivola, Juha
APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban
TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/722,440
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/252,063
PRIOR APPLICATION NUMBER: 09/252,063
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 10
SOPTMARE: Patentin Ver: 2.0
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TYPE: PRT
ORGANISM: Oryctolagus cuniculus
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1 QARQNLQNLFINFCLILLICLLLICIIVMLL
                                                                                             Similarity
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                                                                            Conservative
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                                                                                           100.0%; Score 150; DB 4; 100.0%; Pred. No. 4.4e-13;
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APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Vilgrentula-Ikonen, Marjo
APPLICANT: Lotta, Timo
APPLICANT: Lotta, Timo
APPLICANT: Kalvola, Juha
TITLE OF INVENTION: Carola
TITLE OF INVENTION: Ca-AFFase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION UNMBER: US/09/252,063
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER FILING DATE: 1997-09-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
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US-09-252-063-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-252-063-1
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LENGTH: 52
TYPE: PRT
ORGANISM: Mus 6
US-09-722-440-6
GENERAL INFORMATION:

APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Tenhunen, Jukka
APPLICANT: Vidgren, Jukka
APPLICANT: Yligerttula-Ikonen, Marjo
APPLICANT: Tilgmann, Carola
                                                                                                                                         Sequence 2, Application US/09252063 Patent No. 6538022
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FILE REFERENCE: 1102.0250001

CURRENT APPLICATION NUMBER: US/09/722,440

CURRENT FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: 09/252,063

PRIOR APPLICATION NUMBER: 09/252,063

PRIOR FILING DATE: 1999-02-18

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                 96.0%;
96.7%;
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Pred. No. 2.7e-12;
0; Mismatches 1
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RESULT 14
US-09-722-440-2
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US-09-722-440-1
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; ORGANISM: Sus
US-09-252-063-2
                                                                                            GENERAL INFORMATION:
                                                                                                           Sequence 2, Application US/09722440 Patent No. 6774103
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Best Local Similarity 96.7%;
Matches 29; Conservative
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LENGTH: 52
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LENGTH: 52
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TITLE OF INVENTION: Co-mpounds for Deactivating Phospholamban Function on
TITLE OF INVENTION: Co-ATPase (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/252,063
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 08/937,117
EARLIER FILING DATE: 1997-09-24
NUMBER OF SEQ 1D NOS: 10
NOS: 10
SOFTWARE: Patentin Ver. 2.0
APPLICANT:
                                   APPLICANT: Pollesello, Pie
APPLICANT: Ovaska, Martti
APPLICANT: Tenhunen, Jukk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kaivola, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
TITLE OF INVENTION: CA-ATPASE (Phospholamban Inhibitors)
FILE REFERENCE: 1102.0250001
CURRENT APPLICATION NUMBER: US/09/722,440
CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pollesello, Piero
APPLICANT: Ovaska, Martti
APPLICANT: Tenhunen, Jukka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/252,063 PRIOR FILING DATE: 1999-02-18
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Vidgren, Jukka
Tenhunen, Jukka
Vidgren, Jukka
Yliperttula-Ikonen, Marjo
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Tilgmann, Carola
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96.7%;
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Pred. No. 2.7e-12;
                                                                                                                                                                                                                                                                                                              Score 144; DB 4; Length 52; Pred. No. 2.7e-12;
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APPLICANT: KAIVOIA, Juha
TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
ITITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
ITITLE OF INVENTION: Compounds for Deactivating Phospholamban Inhibitors)

FILE REFERENCE: 1102.0250001

CURRENT APPLICATION NUMBER: US/09/722,440

CURRENT FILING DATE: 2000-11-28

PRIOR RIPLICATION NUMBER: 09/252,063

PRIOR FILING DATE: 1999-02-18

NUMBER OF SEQ ID NOS: 10

SOPTWARE: PATENTIN Ver. 2.0

SEQ ID NO 2

LENGTH: 52

TYPE: PRT
ORGANISM: Sus sp.

US-09-722-440-2
                                                                                                                                                                                                                                                                                                                                                         GENERAL INCOGNATION:
GENERAL INCORNATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION UNMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7310
LENGTH: 89
TYPE: PRT
ORGANISM: Human
US-09-949-016-7310
Search completed: July 7, 2005, 15:44:07 Job time : 91 Becs
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US-09-949-016-7310
; Sequence 7310, Application US/09949016
; Patent No. 6812339
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Best Local Similarity
Matches 29; Conserv
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                      Score
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1: /cgn2_6/ptodata/1/pubpaa/U
2: /cgn2_6/ptodata/1/pubpaa/U
3: /cgn2_6/ptodata/1/pubpaa/U
4: /cgn2_6/ptodata/1/pubpaa/U
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.: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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         GenCore version 5.1.6 (c) 1993 - 2005 Compugen
                                                 6 US-10-724-532-1
US-09-954-571-3
US-09-954-571-4
4 US-10-371-101-14
4 US-10-371-101-15
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US-09-954-571-1
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Sequence 3, Appli
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Sequence 5, Appli
Sequence 14, Appl
Sequence 15, Appl
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Sequence 2, Appli
Sequence 2, Appli
Sequence 478, App
Sequence 1, Appli
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	-10-495-1	-10-495-148-4	-10-282-122A-45	0-104-047	-10-437-963-175	-10-723-860-38	-09-769-736-	-10-282-122A-736	-10-767-701-4223	-10-760-721-	-10-760-721-	-10-101-001-1	-10-161-205-1	-09-491-614-1	-09-259-658-1	-10-760-721-	-10-760-721-	-10-760-721-	-10-873-594-2	US-10-877-930-25	-10-815-514-2	-10-873-594-	-10-877-930-	US-10-815-514-7	-10-724-532-	-10-705-791-	-10-705-791-	-10-705-79	-10-705-791-1	-10-705-791-	-10-705-791-	-10-705-791-	US-10-705-791-3
Sequence 7, Appli	æ	equence 43, Ap	727,	equence 3554,	equence 17	e 38	equence 34	e 73	equence 42	equence 5,	e 6,	æ	equence 17	equence 18	e 19	e J	e 2,	04,	e 25,	e 25,	e 25,	7,	7,		'n	19,	2	18,	17,	6,	5	Sequence 4, Appli	ω,

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RESULT 2

US-09-954-571-3

; Sequence 3, Application US/09954571

; Publication No. US20020032167A1
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                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10724532
Publication No. US20040203027A1
GRMERAL INFORMATION:
APPLICANT: Reed, Thomas D
                                                                                                                                                                                                 Query Match 100.0%; Score 150; DB 16; Best Local Similarity 100.0%; Pred. No. 2.2e-11; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic TITLE OF INVENTION: Reticulum FILE REFERENCE: SR RPA
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TYPE: PRT
; ORGANISM: Canis familiaris
US-09-954-571-3
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APPLICATE: IKEG, YASUhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
SEQ ID NO 3
                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                 Sequence 5, Application US/09954571 Publication No. US20020032167A1
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Best Local
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Best Local Similarity
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APPLICANT:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ROSS, John
APPLICANT: Ikeda, Yasuhiro
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.2
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APPLICANT: Hoshijima, Masahiko
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APPLICANT: Hoshijima, Masahiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 52
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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ilarity 100.0%;
Conservative 0
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Conservative 0
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Pred. No. 3.7e-11;
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Pred. No. 3.7e-11;
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                                                                GENE TRANSFER
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APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590,70035.US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
                                                                                                                                                                                                                                                            US-10-371-101-15
Sequence 15, Application US/10371101
Publication No. US20030149995A1
GENERAL INFORMATION:
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US-10-371-101-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR APPLICATION NUMBER: 099549,872
PRIOR APPLICATION NUMBER: 099549,872
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APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: DO0590.70035.US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zwaal,
APPLICANT: Groene
APPLICANT: Bogaer
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PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 39
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Pred. No. 3.7e-11;
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; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PATENTIN VEY: 2.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: PRT
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US-09-954-571-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Slovic, Avram M.
APPLICANT: Summa, Christopher M.
APPLICANT: Summa, Christopher M.
APPLICANT: Saven, Jeffery G.
APPLICANT: DeGrado, William F.
APPLICANT: DeGrado, William F.
APPLICANT: Kono, Hidetoshi
TITLE OF INVENTION: Computational Design of a Water-Soluble Analog of a Protein, such
TITLE OF INVENTION: See Phospholamban and Potassium Channel KCSA
FILE REFERENCE: 1694.0540001
CURRENT APPLICATION NUMBER: US/10/760,721
CURRENT FILING DATE: 2004-01-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 53
TYPE: PRT
ORGANISM: Canine PLB
                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09954571 Publication No. US20020032167A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10760721 Publication No. US20040215400A1
                     SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 52
TYPE: PRT
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Best Local Similarity
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                                                                                                   APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijam, Masahiko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
ORGANISM: Artificial
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Sequence 478, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Fahy, Eoin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Marnock, Dale B.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 478
LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
ITTLEOANT: Reda, Yasuhiro
ITTLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION UNMBER: US/09/954,571
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/231,821
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
NUMBER OF SEQ ID NOS: 5
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SEQ ID NO 2
LENGTH: 52
TYPE: PRT
RCANISM: Homo sapiens
US-09-954-571-2
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; OTHER INFORMATION: Mutant form of humam protein sequence US-09-954-571-1
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US-10-408-765A-478
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                                                                           ; ORGANISM: Homo sapiens 
US-10-408-765A-478
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Matches
Query Match
Best Local Similarity 96.7
Matches 29; Conservative
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Publication No. US20020032167A1
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Best Local Similarity
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ilarity 96.7%;
Conservative
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96.7%;
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Score 144; DB 16;
Pred. No. 2e-10;
0; Mismatches 1;
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Pred. No. 2e-10;
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Pred. No. 2e-10;
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US-10-705-791-3
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; ORGANISM: Homo sapiens
US-10-705-791-1
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US-10-705-791-1
                APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
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APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
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Best Local
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                            APPLICANT: The Regents of the University of California APPLICANT: Chien, Kenneth APPLICANT: Dillmann, Wolfgang APPLICANT: Minamisawa, Susanne APPLICANT: He, Husping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/106,718
PRIOR PILING DATE: 1998-11-02
PRIOR PILING LOTE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
CURRENT FILE 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
CURRENT FILING DATE: 2003-11-10
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PatentIn version 3.2
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Minamisawa, Susanne
                                                                                                                                                                                                                                                                         Meyer, Markus
                                                                                                                                                                                                                                    Wang, Yibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoshijima,
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Pred. No. 2e-10;
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-4
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US-10-705-791-4
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LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
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SEQ ID NO 4
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Best Local Similarity 96.7
Matches 29; Conservative
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Best Local Similarity
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CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: METHOD FOR INHIBITION OF CARDIAC DISEASE
                                                                APPLICANT:
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Meyer, Markus
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                                            Scott, Chris
Wang, Yibin
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THOD FOR INHIBITION OF
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96.7%;
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Pred. No. 2e-10;
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Pred. No. 2e-10;
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APPLICANT: Hoshijima, Masanıko
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT FILING DATE: 1903-11-10
PRIOR APPLICATION NUMBER: 60/106,718
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
INMHEER OF SEQ ID NOS: 19
SOFTWARE: PAT ON SEQ ID NOS: 19
SOFTWARE: PAT ONS: 19
SOFTWARE: SEQ ID NOS: 19
SOFTWARE: SEQ ID NOS: 19
TYPE: PRT
ORGANISM: Homo sapiens

OC 04. Score 144; DB 16; Length 52;
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; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEO ID NOS: 19
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PAT
; ORGANISM: Homo sapiens
US-10-705-791-5
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Search completed: July 7, 2005, 16:12:48 Job time: 386 secs
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US-10-705-791-6
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Matches 29; Conserv
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Publication No. US20040121942A1
GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                    ch 96.0%; Score 144; DB 16; Length 52; Il Similarity 96.7%; Pred. No. 2e-10; 29; Conservative 0; Mismatches 1; Indels
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Hoshijima, Masahiko
Meyer, Markus
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Listing first 45 summaries
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-QC/Cgn2 1/USPTO_spool/US10724532/runat_07072005_100329_19987/app_query.fasta_1.199
-QC/Cgn2 1/USPTO_spool/US10724532/runat_07072005_100329_19987/app_query.fasta_1.199
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10724532_@CGN 1 4200_@runat_07072005_100329_19987 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPOP=6
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Patent: JP 2002541859-A 9 10-DEC-2002;
DEVGEN NV
OS Sus sp. (pig)
PN JP 2002541859-A/9
PN JP 2002541859-A/9
PD 10-DEC-2000 JP 2000612503
PF 14-APR-2000 JP 2000612503
PF 14-APR-1999 GB 9908670.4,15-APR-1999 US
O1-UUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C1201/42,C12N15/09,C12Q1/02,C12N15/00
CC Method for screening compounds
FH Key Location/Qualifiers
FT source 1. 159
FT source (pig)'.
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Zwaal,R., Groenen,J. and Bogaert,T.
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AV514751 Canis fam
S95849 Rattus sp.
BC061097 Mus muscu
X71068 R.norvegicu
X15075 Pig mRNA fo
M16012 Canine card
M35393 Dog cardiac
M63601 Rabbit phos
S44792 phospholamb
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Y00761 O.cuniculus
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BC005269 Homo sapi
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AC097916 Mus muscu
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AC128365 Rattus no
AC128365 Rattus no
CQ447405 Sequence
M60411 Human phosp
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AP177764 Homo sapi
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PI RICHARD ZWA
PC C1201/42,C1
CC Description
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Zwaal,R., Groenen,J. and Bogaert,T.
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C12Q1/42,C12N15/09,C12Q1/02,C12N15/00
Description of Artificial Sequence:HUMANIZED
Location/Qualifiers
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Zwaal,R., Groenen,J. and Bogaert,T.
Compound screening methods
Patent: US 6540996-A 13 01-APR-2003;
Location/Qualifiers
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Zwaal,R., Groenen,J. and Bogaert,T.
Compound screening methods
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Compound screening methods
Patent: WO 0063426-A 13 26-OCT-2000;
Devgen NV (BE)
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Rattus sp.
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
                                           21
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Cloning phospholamban cDNA from rat aortic
Adv. Exp. Med. Biol. 304, 387-395 (1991)
92206263
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S95853
S95853.1 GI:247932
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                                                                   GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
                                     LeuLeuIleCysIleIleValMetLeuLeu 30
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                        CTGCTGATCTGCATCATTGTGATGCTTCTG
                                                                                                                                                                                                                                             /codon_start=1
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ICIIVMLL"
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                                                                                                                                                                                                                                                                                                                   'note="PLN"
                                                                                                                                                                                                                                                                                                                            gene="phospholamban, PLN"
                                                                                                                                                                                                                                                                                                                                                   gene="phospholamban,
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                                                                                     106 CAAGCACGTCAAAATCTTCAGAACCTATTTATAAATTTCTGTCTCATTTTAATATGTCTC
                            166
                                                      21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 314)
Housley, D.J.E., Ritzert, E. and Venta, P.J.
Comparative radiation hybrid map of canine
incorporating SNP and indel polymorphisms
Genomics 84 (2), 248-264 (2004)
2 (bases 1 to 314)
Housley, D.J.E., Ritzert, E. and Venta, P.J.
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Canis familiaris phospholamban
AY514751
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Mammalia;
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                                             LeuLeuIleCysIleIleValMetLeuLeu
                              TTGTTGATCTGCATCATTGTGATGCTTCTC
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199. .>314
/gene="PLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="sequence information was obtained from a pool of
ten breeds: German shepherd dog; Beagle; German shorthair
pointer; Scottish terrier; Doberman pinscher; Greyhound;
Siberian husky; Labrador retriever; Collie; Cocker
spaniel; additional sequence was obtained from a single
mixed breed dog of unknown origin"
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                                                                                                                                                                                                                                                                                                                                                 /gene="PLN"
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/translation="MDKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="PLN"
/number=2
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Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          product="phospholamban"
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State University,
MI 48824-1314, USA
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Canis.
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Rattus
S95849
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausmer, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Bhat, N.K., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
                                                                                                                                                                                                                                                                                                                            H
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Hwang, K.S. and Nadal-Ginard, B.
Cloning phospholamban cDNA from rat aortic
Adv. Exp. Med. Biol. 304, 387-395 (1991)
                                                    Mammalia; Eutheria;
1 (bases 1 to 648)
                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                           Mus musculus (house mouse)
                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenBank staff at the National Library of Medicine cuentry [NCBI gibbsq 95849] from the original journal
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                                                                                                                                                              IMAGE: 6772294),
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Eutheria;
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|CIIVMLL"
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/db_xref="GI:26986719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Pln"
59. .317
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db_xref="taxon:10118"
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Rodentia;
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Conservative:
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                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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(cDNA clone MGC:74215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAL Plate: 53 Row: g Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12963502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (03-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcc@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Dr. Jonathan Kuo, NIMH cDNA Library Preparation: Michael Brownstein / Ted Usdin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                                                                                                                                                                            /codon_start=1
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/protein_id="AAH61097.1"
/db_xref="GI:38173947"
/db_xref="LocusID:18821"
/db_xref="MGI:97622"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: PLB"
/db_xref="LocusID:18821"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mol_type="maxin:
/db_xref="taxon:1090"
/clone="MGC:4215 IMAGE:6772294"
/clone="MGC:4215 mouse"
                                                                                                                                                                                                                                                                                                                                                                      'gene="Pln"
                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="MGI:97622"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Pln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="Vector: pDNR-LIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="Testis, mo/clone_lib="NIH_MGC_169"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                   translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL"
   4.17e-09
   648
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RNPHLAMB
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US-10-724-532-1 (1-30) x RNPHLAMB (1-701)
                                                                                          Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shanahan, C.M., Weissberg, P.L. and Metcalfe, J.C. Isolation of gene markers of differentiated and proliferating vascular memoch muscle cells Circ. Res. 73 (1), 193-204 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (26-FEB-1993) C.M.
Dept of Biochemistry, Tennis
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phospholamban.
Rattus norvegicus (Norway rat)
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Direct Submission
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                                                                                                                                                                                                                            /product="phospholamban"
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/db_xref="GI:313810"
                                                                                                                                                                   /db_xref="GOA:P20006"
/db_xref="Uniprot/Swibs-prot:P20006"
/translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINPCLILICLLL
ICIIVMLL"
                                                                                                                                                                                                                                                                                                                                                                                                organism="Rattus"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                          /dev_stage="adult"
L74. .332
                                                                                                                                                                                                                                                                                                                     tissue_type="aorta smooth muscle"/clone_lib="lambda-Zap"
                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                     clone="2RB7"
                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                   strain="Wistar"
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GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu

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Submitted (13-APR-1989) Eggermont J.A., Laboratorium Voor
Fysiologie K.U. Leuven, Campus Gasthuisberg O/N, Herestraat 49,
B-3000 Leuven, Belgium
See < 100399> for canine phospholamban and < 100761> for rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Verboomen,H., Wuytack,F., Eggermont,J.A., De Jaegere,S., Missiaen,L., Raeymaekers,L. and Casteels,R. cDNA cloning and sequencing of phospholamban from pig stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSPLB 73
Pig mRNA for phospholamban.
X15075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phospholamban.
Data kindly re
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Eggermont, J.A.
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                                            GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu
  LeuLeuIleCysIleIleValMetLeuLeu
                               CAAGCACGTCAAAACCTTCAGAACCTATTTATCAATTTCTGTCTCATCTTAATATGCCTC
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                                                                                                                                                                                                                                                             /note="pot.polyA signal"
737
                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAA33171.1"
/db_xref="GI:2056"
                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="smooth muscle"
/clone_lib="lambda_gt11"
/dev_stage="2-day-old piglet"
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                                                                                                                                                                                                                                                                                                                  /db_xref="UniProt/Swiss-Prot:P07473"
/translation="MDKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL
                                                                                                                                                                                                                                                                                                                                                                                                      note="unnamed protein product;
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                                                                                                                                                                                                                                               'note="polyA site"
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                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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'db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Sus scrofa"
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Cetartiodactyla; Suina; Suidae;
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Sus.
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                                                                                                                                              Canis sp.
                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoscon Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 832)

Uyeda,A., Kitano,K., Fujii,J., Kadoma,M., Tada,M. and Tanaka,S. Characterization of recombinant cDNA clones for canine cardiac
                                                                                                                                                                                                   B32 bp
Dog cardiac phospholamban mRNA,
M35393
                                                                                                                                                                                                                                                                                                                                                                            μ,
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Fujii,J., Ueno,A., Kitano,K., Tanaka,S., Kadoma,M. a Complete complementary DNA-derived amino acid sequen cardiac phospholamban J. Clin. Invest. 79 (1), 301-304 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phospholamban.
Canis lupus (gray wolf)
Canis lupus
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M16012
 Original
                                            Nucleic Acids
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                                                                                                                                                                                        M35393.1 GI:164045
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Location/Qualifiers
                                                          phospholamban
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  source text:
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ICIIVMLL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="cardiac phospholamban"
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Canis.
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Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 858)
Fujii,J., Zarain-Herzberg,A., Willard,H.F., Tada,M. and
MacLennan,D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rabbit phospholamban gene, partial exon M63601 GI:165636 phospholamban gene, partial exon M63601.1 GI:165636
                                                                                                                                                                                                                                                                                                                                        Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6 J. Biol. Chem. 266 (18), 11669-11675 (1991) 91268032
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGITGATCIGCATCATTGIGATGCTTCTC 336
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CTGCTGATCTGCATCATCGTCATGCTTCTC 679
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Search completed: July 7, 2005, 18:51:24 Job time: 8380 secs

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-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10724532 @CGN 1 1 4352 @runat 07072005 100329 19999 -NCPU=6 -ICPU=3
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AAB39963 VW66E09.r

AA655419 VV14D04.r

BY149365 BY149365

AA433518 Vf42E04.r

BY068506 BY068506

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2 um63b05.y	226	2689	N	4	8	150	ω
8 vg12f03.x	481	138	Ļ	4	80.	150	N
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ALIGNMENTS

UI-R-BJI-awe-d-04-0-UI.81 UI-R-BJI Rattus norvegicus cDNA clone UI-R-BJI-awe-d-04-0-UI 3', mRNA sequence. BE113353.1 GI:8505458 ESTI. BE113353.1 GI:8505458 ESTI. Rattus norvegicus (Norway rat) Rattus norvegicus (Chordata; Craniata; Vertebrata; Euteleostomi; Rattus norvegicus Rattus norvegicus Rattus norvegicus Rattus 1 to 179) Rattus I (bases 1 to 179) Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene discovery Genome Res. 6 (9), 791-806 (1996) 97044477 Contact: Soares, MB Contact: S
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                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                             Waterston,R.
The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                       Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dul
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 209)
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5' similar to
Trace considered overall poor quality
                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-BJ1"
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to gb:M63603
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                                                                                  Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lu
                                                                                                                                                                                                           1 (bases 1 to 328)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubux, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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vw66f09.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
IMAGE:1259945 5' similar to gb:M63603 CARDIAC PHOSPHOLAMBAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further;
                                                                                                                                                                            Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                      AA839963.1 GI:2916557
                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMAN);,
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/lab_host="DH10B"
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/clone="IMAGE:871527"
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/strain="C57BL/6J"
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                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Pax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 331)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
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                                                       Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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AA655419.1 GI:2591573
EST.
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Location/Qualifiers
MGI:647943
Seq primer: -28ml3 revl ET from Amersham
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/dev_stage="13 day embryos"
/lab host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/clone_lib="Stratagene mouse heart (#937316)"
/note="Forgan: heart; Vector: pBluescript SK-; Site_1:
/note="Forgan: heart; Vector: pBluescript SK-; Site_1:
/note="Forgan: heart; Vector: plus contail to the contail to 
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/mol_type="mRNA"
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/clone="IMAGE:1259945"
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RS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Belsel,K.W., Blake,J.A., Bradt,D., Brust,C., Corbani,L.B., Cousins,S., Dalla,E., Dragani,T.A., Chothia,C., Corbani,L.B., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kansi,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Nunata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Nunatais,L., Marchonni,L., McKenzie,L., Miki,H., Nagashima,T., Petrovsky,N., Pillai,R., Pontius,J.U., Oj,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wajner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Vang,L., Yang,I., Yang,I., Yang,I., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
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BY149365 RIKEN full-length enriched, 17.5 days embryo whole body Mus musculus cDNA clone L930261L14 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
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/dev_stage="13 'day embryos"
/dev_stage="13 'day embryos"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse heart (#937316)"
/clone="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note=
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/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:1211599"
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1777-1771 (2000)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome
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/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryowhole body"
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                    μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Porest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuc
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 271.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA433518.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 347)
                           GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu
provided by
                                                                                                                                                                                                                                                                                    constructed
                                                                                                                                                                                                                                                                                                      3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE:846463"
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to gb:M63603
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NbMH Mus musculus cDNA clone IMAGE:846463
CARDIAC PHOSPHOLAMBAN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                      normalized by Bento Soares and M. Fatima
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RESULT 7
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                                                                                                                                               Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y., Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-171 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rogers,J., Birney,E. and Hayasnızakı,:.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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Fax: 81-45-503-9216
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                                 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construncedundant cDNA library. Genome Res. 11 (2), 281-289
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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cDNA library was prepared and sequenced in Mouse Genome
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 362)

Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M.,
                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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BY770786 RIKEN full-length enriched, 17.5 days embryo whole body
Mus musculus cDNA clone L930045G09 5', mRNA sequence.
BY770786
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Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome
                                                                           Tel: 81-45-503-9222
                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
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Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                     Fax: 81-45-503-9216
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/clone_lib="RIKEN full-length enriched, 17 days embryo
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/strain="C57BL/6J"
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AI597561
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Query Match:
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                   FEATURES
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                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 366)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                             Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI597561 366 bp mRNA linear EST 21-APR-19 vd80e10.y1 Soares mouse NbMH Mus musculus cDNA clone IMAGE:806922 5' similar to gb:M63603 CARDIAC PHOSPHOLAMBAN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                               MGI:483266
This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in )
                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further details.
                                                           correct orientation
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                                       primer: -40RP from Gibco
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/clone ___
--le body"
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/dev_stage="17.5 days embryo"
/clone_lib="RIKEN full-length enriched, 17.5 days embryo
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/mol_type="mRNA"
/strain="C57BL/6J"
                 Location/Qualifiers
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-fr
IMAGE Consortium (info@image.llnl.
                                                                                             Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina; (bases 1 to 369)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubgeisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Theising, B., Wylie, T., Lemnon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vg05g01.rl
5′ similar
High quality sequence stop: 320
Location/Qualifiers
                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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/lab_host="DH10B"
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/sex="male"
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/strain="C57BL/6J"
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to gb:M63603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 bp mRNA linear EST 01-JI NDMH Mus musculus cDNA clone IMAGE:8 CARDIAC PHOSPHOLAMBAN (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus"
                                                   royalty-free through LLNL ; contact the image.llnl.gov) for further information.
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Matches:
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on, R. and
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Contact: Addlson F. da Mota
Contact: Addlson F. da Mota
Gene Evaluation and Mapping Laboratory
USDA, ARS, Animal and Natural Resources
Bldg. 200 Rm3 BARC-East, Beltsville, MD
Tel: 3015048456
Fax: 3015048414
                                                                                                                                                                                              1 (bases 1 to 373)
dd Mota,A.F., Sonstegard,T.S., Van Tassell,C.P., Matukumalli,L.K.,
Wood,D.L., Capuco,A.V., Brito,M.A.P., Martinez,M.L., Connor,E.E.,
Machado,M.A. and Coutinho,L.L.
Construction and Characterization of cDNA Libraries Generated from
Mammary Gland Tissues of Holstein (Bos taurus) and Gir (Bos
                                                                                                                                                                                                                                                                                                  Bos indicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                                                                                                                                                                                                                                                  Unknown, mRNA sequence.
CB041339
CB041339.1 GI:27760584
EST.
Email: amota@cnpgl.embrapa.br
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '' -trim_fasta. Vector identified
by cross_match using options -minmatch 12 -minscore 12
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                                                                                                                                                                                  indicus) Cattle
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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CE 1 (bases 1 to 375)

RS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K. S., Gassterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
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BY092385 RIKEN full-length enriched, 10 days neonate heart
musculus cDNA clone K630091G17 5', mRNA sequence.
BY092385
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High quality sequency of the sequency of
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone lib="BARC-EMBRAPA 312BOV"
/note="Organ: mammary; Vector: pUC19; Site 1: SmaI;
Site 2: SmaI; This mammary-derived cDNA 11brary was
created as part of a collaborative project between the AR
Gene Evaluation and Mapping Laboratory and the EMBRAPA
Dairy Cattle Research Center under the sponsorship of
USDA, ARS/EMBRAPA-LABEX program in animal genomics RNA
extracted on 6/8/02 with Invitrogen Superscript II at 37
deg C annealing temperature."
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/cell_type="multiple"
/dev_stage="involuted"
/lab_host="K-12"
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/clone="312BOV_1A09"
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/mol_type="mRNA"
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strain="Brazilian Dairy
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                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazzki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-163 (1000)
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Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="heart"
/dev_stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgerThis clone is also available through the I.M.A.G.E. Consortium LLNL (inf@@image.llnl.gov). IMAGE ID= 1789595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 5224:
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UI-R-C2p-rc-e-01-0-UI.rl UI-R-C2p Rattus norvegicus
UI-R-C2p-rc-e-01-0-UI 5', mRNA sequence.
BF64730
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/note="Vector: pT773D-Pac (Pharmacia)
/note="Vector: pT773D-Pac (Pharmacia) with a modified
/note="Vector: pT773D-Pac (Pharm
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Consortium at
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length.
                                                                                                                                                                                                                                                                                                               FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTATAGG
Insert Length: 378 Std Error: 0.00
Plate: BP250001B10 row: F column: Seq primer: AGCGGATAACAATTTCACACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Fax: 217 244 5617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Lewin, H. A. Omparative and Functional Genomics W. M. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana,
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BF044741.1 GI:10761796
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                                                                                                                                                                                                                                                                            quality sequence stop: 378.
Location/Qualifiers
/lab_host="DH10B"
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Site_2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lemnon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. "
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                                                                                                                                                                                                                                  organism="Bos taurus"
                                                                                                                                                   'sex="female"
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Bikaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Rikaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Riyoses 1 to 378)

Riyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wang, Y., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wang, J., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninnoi, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Bitray, E. and Hayashizaki, Y.,
Sasaki, Y.,
Sasaki, Y.,
Sander, S., Sasaki, D., Shibata, K.,
Shibata, K.,
Shibata, Y.,
Shibata, Y
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                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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BY088220 RIKEN full-length enriched, 10 days neonate heart Mus musculus cDNA clone K630069L15 5', mRNA sequence.
                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
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genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Search completed: July 7, 2005, 19:27:09 Job time: 2144 secs
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Pred. No.:
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Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
                                                                                                                296
                                                                                                                                                                                                                        236 CAAGCACGTCAGAATCTCCAGAACCTATTTATCAATTTCTGCCTCATCTTGATATGTCTG
                                                                                                                                             21 LeuLeuIleCysIleIleValMetLeuLeu 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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                                                                                                                CTGCTGATCTGCATCATTGTGATGCTTCTG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
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Result
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Ggn2 _1/USPTO_spool/US10724532/runat_07072005_100330_20013/app_query.fasta_1.199
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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/cgn2 6/ptodata/1/ina/6A COMB.seq:*
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US-09-549-872B-13

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US-09-949-016-133

US-09-949-016-13181

US-09-949-016-15638

US-09-270-767-10524

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Sequence 9, Appli
Sequence 13, Appl
Sequence 10799, A
Sequence 1439, Ap
Sequence 26, Appl
Sequence 15638, A
Sequence 10524, A
Sequence 11139, A
Sequence 14599, A
Sequence 12461, A
Sequence 12461, A
Sequence 16853, A
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ALIGNMENTS

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US-09-549-872B-9
; Sequence 9, Application US/09549872B
; Patent No. 6540996
; GRNERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D0590/70008 (JRV/RE)
CURRENT FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 1999-04-15
PRIOR RILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR PILING DATE: 1999-06-01
INUMBER OF ESQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 159
CORGANISM: Sus sp.
US-09-549-872B-9

Alignment Scores:
Pred. No.:
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PRIOR APPLICATION NUMBER: GB 9912736.7
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PRIOR FILING DATE: 1999-04-15
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US-10-724-532-1 (1-30)

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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-04
PRIOR FILING DATE: 1999-05-01
PRIOR FILING DATE: 1999-05-01
PRIOR FILING DATE: 1999-05-01
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             APPLICANT: Duclert, A.
APPLICANT: Siordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59. US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
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                                                                                                                                                                                                                                                                    Sequence 10799, Application US/09513999C Patent No. 6783961
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                                                                                                                                                                                        APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
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APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Matches:
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CL001307
CURRENT FILING DATE: L000-04-14
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASESEQ FOR Windows Version 4.0
SEQ ID NO 1439
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; TYPE: DNA
; ORGANISM: Homo sai
US-09-513-999C-10799
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                                                         US-09-949-016-13181; Sequence 13181, Ap; Patent No. 6812339
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                 GENERAL INFORMATION:
APPLICANT: VENTER, J.
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TITLE OF INVENTION:
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TYPE: DNA
ORGANISM: Human
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POLYMORPHISMS
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248 CAAGCACGTCAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCATCTTAATATGTCTC
             1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
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Mismatches:
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Mismatches:
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ASSOCIATED

307

FILE REFERENCE:

CL001307

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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Sequence 26, Application US/09124671A

Patent No. 6160088

GENERAL INFORMATION:
APPLICANT: Mayhew, Mark
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
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Best Local Similarity:
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TYPE: DNA
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                                   100 CAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCATCTTAATATGTCTCTTGCTGATC
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; ORGANISM: Drosophila melanogaster
US-09-270-767-10524
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Percent Similarity:
Best Local Similarity:
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEG ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEG ID NO 10524
LENGTH: 490
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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SEQ ID NO 15638
LENGTH: 69764
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(69764)
OTHER INFORMATION: n = A,T,C
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RESULT 10
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DB:
Query Match:
             Percent Similarity:
Best Local Similarity:
                                                                      Alignment Scores:
                                                                                                   US-09-270-767-14599
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                                                                                                               SEQ ID NO 14599
LENGTH: 992
TYPE: DNA
ORGANISM: Drosophila melanogaster
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Patent No. 6703
                                                                                                                                                                                                                                                                          Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     Sequence 14599,
                                                                                                                                                                       APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
NUMBER OF SEQ ID NOS: 62517
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TYPE: DNA
ORGANISM: Drosophila melanogaster
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US-09-949-016-16853
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US-09-949-016-12461
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SOFTWARE: FastSEQ for
SEQ ID NO 12461
                                                                                                                                                                                                                                                         Sequence 16853, Applica
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J.
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GENERAL INFORMATION:
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                                                         CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                      APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-39
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 136216
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-136216
US-09-949-016-15563
; Sequence 15563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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US-09-949-016-136216/c
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SEQ ID NO 16853
LENGTH: 93920
TYPE: DNA
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                              Local Similarity:
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR REPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 15563
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Best Local Similarity:
Query Match:
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; NAME/KEY: misc feature
; LOCATION: (1)...(202001)
; OTHER INFORMATION: n = A,T,C
US-09-734-674-3
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US-10-724-532-1 (1-30) x US-09-734-674-3 (1-202001)
                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-734-674-3/c
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; LENGTH: 202001
; TYPE: DNA
; ORGANISM: Human
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Patent No. 6498022

GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui et al

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL001018

CURRENT APPLICATION NUMBER: US/09/734,674

CURRENT FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
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ORGANISM: Human
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Search Job ti	Db	Ş	ğ
Search completed: July 7, 2005, 19:36:16 Job time : 550 secs	92176 GTC 92174	27 Val 27	92236 CAAAATTCATTTCTGTCTTTTGTATTATTTTTTTTTACTAAAATATGTTTGCCTTCTG 92177
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Wed Jul 13

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Run
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-Q-(gn2 1)/USPTO spool/US10724532/runat 07072005 100331 20083/app query.fasta_1.199
-DBs-Published Applications NA -QFMT=fastap SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANUS=hunan40.cdi -LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10724532 @CGN 1 741 @runat 07072005 100331 20083
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NGE SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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/ Cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
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/ Cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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453.854 Million cell updates/sec
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n2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
n2_6/ptodata/1/pubpna/PCG_NEW_PUB.seq:*
n2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
n2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
n2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
n2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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,		280	quence 4970,	255,		501,	649,	3, AL	Sequence 1	Sequence	Sequence 303, Appli	equence 5	199,	Sequence 247, App	equence 53889		17377,	e 26, App	Sequence 26, Appl	equence 5,	• •	e 52	Sequence 3950, A	equence 42	თ.თ	equence 4045, A	Sequence 13, Appl Sequence 1, Appli	equence 9, Appl	ription

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Sequence 13, Application US/10371101

Publication No. US20030149995A1

GENERAL INFORMATION:

APPLICANT: Zwaal, Richard

APPLICANT: Groenen, Jose

APPLICANT: Bogaert, Thierry

TITLE OF INVENTION: COMPOUND SCREENING METHODS

FILE REFERENCE: D00590.70035.US

CURRENT APPLICATION NUMBER: US/10/371,101

CURRENT FILING DATE: 2003-02-21

PRIOR APPLICATION NUMBER: US 60/129,596

PRIOR APPLICATION NUMBER: US 60/129,596

PRIOR APPLICATION NUMBER: GB 9912736.7

PRIOR FILING DATE: 1999-06-01

PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PAFENTIN Ver. 2.0
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; TYPE: DNA
; ORGANISM: Sus sp.
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                                                    US-10-724-532-1 (1-30) x US-10-371-101-13 (1-159)
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                             LENGTH: 159
TYPE: DNA
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APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 2041-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASESSQ for Windows Version 3.0
SEQ ID NO 4045
LENGTH: 525
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; LENGTH: 159
; TYPE: DNA
; ORGANISM: Human
US-10-691-412-1
                                                                                                  ; FEATURE:
, NAME/KEY: misc feature
; LOCATION: (1)...(525)
; OTHER INFORMATION: n =
US-09-918-995-4045
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US-09-918-995-4045
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Query Match:
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Best Local Similarity:
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APPLICANT: Kranias, Evangelia G.
APPLICANT: Kobra, Haghighi
APPLICANT: Kobra, Haghighi
TITLE OF INVENTION: Phospholamban Polymorphisms and Methods of Assessment
FILE REFERENCE: 10738-47
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4045, Application US/09918995
Publication No. US20030073623A1
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Publication No. US20040191802A1
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CURRENT FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                        ORGANISM: Homo sapiens
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APPLICANT: Ebner, Reinhard
APPLICANT: Carter, Kenneth
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR APPLICATION NUMBER: U.S. 60/245,084
PRIOR APPLICATION NUMBER: U.S. 60/245,084
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Best Local Similarity:
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US-10-843-641A-162
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-162
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US-09-873-367C-162
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Sequence 162, Application US/10843641A
Publication No. US20050064454A1
GENERAL INFORMATION:
APPLICANT: Avalon Pharmaceuticals, Inc.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-189
CURRENT APPLICATION NUMBER: US/10/843,641A
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Augustus, Meena
Ebner, Reinhard
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o. US20030165839A1
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GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4217

LENGTH: 394
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Best Local Similarity:
Query Match:
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US-09-918-995-4217
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; ORGANISM: Homo
US-10-843-641A-162
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PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/09/967,768
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/09/968,007
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-02
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Publication No. US20030073623A1
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SEQ ID NO 162
LENGTH: 1635
FEATURE:

NAME/KEY: misc_feature

LOCATION: (1).T.(394)

OTHER INFORMATION: n = A,T,C

-09-918-995-4217
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PRIOR APPLICATION NUMBER: US/09/873,367
PRIOR FILING, DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US/09/954,531
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/09/954,456
PRIOR FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 8447
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PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/09/962,832
PRIOR FILING DATE: 2001-09-25
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                                                                                                                              TYPE: DNA
                                                                                                     ORGANISM: Homo sapiens
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Percent Similarity:
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US-09-918-995-3950
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, NAME/KEY: misc feature
; LOCATION: (1)...(487)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-5377
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US-09-918-995-5377
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GENERAL INFORMATION:
APPLICANT: HYSEQ, IIIC.
APPLICANT: HYSEQ, IIIC.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
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TITLE OF INVENTION: ROVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 5377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5377, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
                                                                                                                                Sequence 3950, Application US/09918995
Publication No. US20030073623A1
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TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; RAIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5235
; LENGTH: 418
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                                                                                                                                     US-10-724-532-1 (1-30) x US-09-918-995-5235 (1-418)
                                                                                                                                                                                        Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                           Pred. No.:
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US-09-918-995-5235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5235, Application US/09918995 Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(418)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 TTGCTGATCTGTATCATCGNGATGCTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 CAAGCACGTCAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCATCTTAATATGTCTC 307
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                                                                                     GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleCeuIleCysLeu 20
                                LeuLeuIleCysIleIleValMetLeuLeu 30
                                                               CAAGCACGTCAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCATCTTAATATGTCTC
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Matches:
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Mismatches:
Indels:
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US-10-724-532-4/c
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; ORGANISM: mus musculus
US-10-724-532-3
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US-10-724-532-3
                                                  US-10-724-532-1 (1-30) x US-10-724-532-4 (1-108)
                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10724532

Publication No. US20040203027A1

GENERAL INFORMATION:
APPLICANT: Reed, Thomas D

TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo) plasmic TITLE REFERENCE: SR RPA CURRENT APPLICATION NUMBER: US/10/724,532

CURRENT PILING DATE: 2003-11-29

PRIOR APPLICATION NUMBER: US/0/30322

PRIOR FILING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 5 Patentin version 3.2
SEQ ID NO 5 Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10724532 Publication No. US20040203027A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.2 SEQ ID NO 4
                                                                                                                                                                                                                                LENGTH: 108
TYPE: DNA
ORGANISM: mus musculus
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                                                                                                                                                                  No.:
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CTGCTGATTTGCATTATCGTCATGCTCCTG 108
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Query Match:
DB:
                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                      ; TYPE: DNA; organism: mus musculus US-10-724-532-6
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US-10-724-532-6/c
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                                                                                                                                                                                                                                                  Sequence 6, Application US/10724532
Publication No. US20040203027A1
GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-02
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR TILING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOPTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 135
TYPE: DNA
ORGANISM: mus musculus
                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10724532 Publication No. US20040203027A1
                                                                                                                                                                                       LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91
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RESULT 15

US-10-815-514-26

i Sequence 26, Application US/10815514

Publication No. US20040204361A1

i GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Hoe, Mee

TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488

CURRENT FILING DATE: 2004-03-31

PRIOR APPLICATION NUMBER: US/10/815,514

CURRENT FILING DATE: 2000-10-26

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PASTSEQ for Windows Version 3.0

SEQ ID NO 26

LENGTH: 315

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chimeric human PLB-KDEL

US-10-815-514-26
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Best Local Similarity:
Query Match:
Search completed: July 7, 2005, 20:34:06
Job time: 424 secs
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                                                      TGTATCATCGTGATGCTTCTC 180
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: gb_ba:*

2: gb_ht;

3: gb_ir

4: gb_c

5: gb_ir

7: gb
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 seq length: 0
seq length: 2000000000
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Match Length DB
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US-10-724-532-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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1786
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RABPHLAM2
OCPHLAM
BD247907
BD247911
AR302007
AX040487
AX040491
SSPLB
S95853
S95863
RATPHOLAMB
RATPHOLA02
AC0128365
BX276081
BC061097
S46792
AC100317
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M63601 Rabbit phos Y00761 O.cuniculus BD247907 Method fo BD247911 Method fo AR302003 Sequence AX040487 Sequence AX040487 Sequence AX040491 Sequence X15075 Pig mRNA fo S95853 phospholamb S95849 Rattus sp. X71068 R. norvegicu L03382 Rat phospho AC097906 Rattus no AC128365 Rattus no BX276081 Zebrafish BC061097 Mus muscu S46792 phospholamb BC061097 Mus muscu
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30.4	30.4	30.4	30.7	33.3	40.4	41.1	41.1	41.1	41.1	42.6	42.6	42.6		42.6	42.6	42.6	•	42.6	٠	42.6		43.0	43.0	43.3	43.5
2254	1893	1593	204114	147419	315	2614	832	832	314	150290	66092	60797	1691		1635		980	480	480	323	306	3423	3312	133901	177018
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AK125620 Homo sapi	X98294 Homo sapien	AK098521 Homo sapi	AC108810 Mus muscu	AL031736 Human DNA		О	M35393 Dog cardiac	Can	AY514751 Canis fam	Z99496 Human DNA s	АL136974 Ното варі	Homo	Homo	_		CQ718671 Sequence			AX894936 Sequence	_	CQ447405 Sequence	M59038 Chicken pho		S	AC099716 Mus muscu

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ALIGNMENTS

RESULT 1

0 0 0 0

ORIGIN	CDS	mRNA exon	· source	FEATURES	PUBMED	JOURNAL	TITLE	REFERENCE		SOURCE	KEYWORDS	VERSION	DEFINITION	RABPHLAM2
/function="regulatory protein of sarcoplasmic reciculum Ca-ATPase" /codon start=1 /product="phospholamban" /protein id="AAA31445.1" /db_xref="G::165639" /translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL ICIIVMLL"	<pre>iuct="phospholamban" per=2 .682</pre>	join (M63600.1:855943,428858) /product="phospholamban" 428858	/organism="Oryctolagus cuniculus" /mol_type="genomic DNA" /db_xref="taxon;9986" /tieno.ith="restrictions"	Original Source Cext: Kabble DNA. Location/Qualifiers	name to the Table	assignment of the gene to human chromosome 6 Chem. 266 (18), 11669-11675 (1991)	MacLennan, D.H. Structure of the rabbit phospholamban gene, cloning of the human	H	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	Oryctolagus cuniculus (rabbit)		M63601.1 GI:165636	phospholamban gene, partial exon 2.	BS B

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VERSION
KEYWORDS
SOURCE
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SOURCE
ORGANISM
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BD247907
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AUTHORS
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Best Local S
Matches 71
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PUBMED
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Best Local Similarity
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Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                               159 bp Method for screening compounds. BD247907
                                                                                                                                                                                                                                                                                         σ
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 2841)
Fujii, J., Lytton, J., Tada, M. and MacLennan, D.H.
Rabbit cardiac and slow-twitch muscle express the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCPHLAM
O.cuniculus mRNA for
Y00761
                                            de ens
                                                                       BD247907.1 GI:33057677 JP 2002541859-A/9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phospholamban gene FEBS Lett. 227 (1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y00761.1 GI:1661
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Similarity 69.6%;
71; Conservative
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                                                                                                                                                                                                      CTTGATATGTCTCCTGCTGATCTGCATCGTCATGCTTCT 332
                                                                                                                                                                                                                                                                                        TGAGAGAAGGCCTCAGGCCAGGCAGAACCTCCAGAATGCTTTCATTGCTTTTTTGTCTGAT
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="phospholamban"
/protein_id="CAA68730.1"
/protein_id="GA162"
/db_xref="GG1:1662"
/db_xref="GGA:P20006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Oryctolagus
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                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref="UniProt/Swiss-Prot:P20006"
translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL
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phospholamban.
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Pred. No. 2.2e-06;
0; Mismatches 31;
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Pred. No. 2.5e-06;
0; Mismatches 31;
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                 Sus.
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                               Euteleostomi;
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OS Sus sp. (pig)
PN JP 2002541859-A/9
PN JP 2002541859-A/9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PF 15-APR-1999 GB 9908670.4,15-APR-1999 US
O1-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42,C12N15/09,C12Q1/02,C12N15/00
CC Method for screening compounds
FH Key Location/Qualifiers
FT source 1.159
FT source /organism='Sus sp. (pig)'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 CTTAATATGCCTCTTGCTGATTTGCATCATCGTGATGCTTCT
                                                                                                                                                          DEVGEN NV
DEVGEN NV
OS Artificial
PN JP 20025418
PN JP 20025418
PN 10-DEC-2002
PF 14-APR-2000
PR 15-APR-1999
O1-JUN-1999 GB
PI RICHARD ZWA
PC C12Q1/42,C1
CC Description
Key
FT source
FT source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
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Zwaal, R., Groenen, J. and Bogaert, T.
Method for screening compounds
Patent: JP 2002541859-A 13 10-DEC-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BD247911.1 GI:33057681 JP 2002541859-A/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 70; Conserv
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Method for screening compounds
Patent: JP 2002541859-A 9 10-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic construct
synthetic construct
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Method for screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BD247911
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JP 2002541859-A/13
                                                                                                                                                                                                         RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT C12Q1/42, C12N15/09, C12Q1/02, C12N15/00 Description of Artificial Sequence: HUMANIZED
                                                                                                                                                                                                                                                                  14-APR-2000 JP 2000612503
15-APR-1999 GB 9908670
W-1999 GB 9912736.7
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                                                                                                                                      /organism='Artificial
Location/Qualifiers
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68.6%;
                47.0%;
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Score 50.8; DB
Pred. No. 6e-06;
); Mismatches
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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 chosen parameters:
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AACH1683

ACH16835

ABL61825

ADN04087

ADP21384

ACH16738

ACH17005

ACH17005

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Compugen Ltd.
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       Aac64967 Pig phosp
Adb53082 Primary r
Adr97285 Human pho
Abn22344 Human ORF
Aac06724 Human Gec
Ach16833 Human adu
Abl61825 Colon ade
Add04087 Antipsori
Adp21384 Gene PuN
Ach16738 Human adu
Ach16738 Human adu
Ach18023 Human adu
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Ach18023 Human adu
Ach18065 Human adu
Ach1806 Human adu
Ach18070 Human adu
Ach18070 Human adu
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Ads20398 KUBL rece
Ach1630 Human col
Abk83374 Human col
Abk83374 Human col
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Pig phospholamban

09-FEB-2001 AAC64967;

(first entry)

AAC64967 standard;

CDNA; 159

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30	30	30	30	30	30	30.2	30.2	30.4	30.4	31.2	32	32	32	32	32	32	32.8	32.8		32.8	32.8		32.8	
27.8	27.8	27.8	27.8	27.8	27.8	28.0	28.0	28.1	28.1	28.9	29.6	29.6	29.6	29.6	29.6	29.6	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4
415	415	415	415	415	415	639	639	2175	1938	473	10625	10625	6536	6481	6481	6481	3925	3748	3708	3647	3647	3647	3647	2422
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AAK28730	ABA24770	ABA44562	AAI34661	ABA55007	AAI13308	ACF73801	ABT14895	AAX24906	ACN44341	ADQ79072	AAL41031	AAC85836	AAC75801	ADB49166	ADQ99406	AAI59183	ADQ21778	AAC77686	AAZ77530	ACN38837	ADR25399	ADF81412	ABK83658	ADC37617
. Aak28730 Human bon	Aba24770 Probe #32	Aba44562 Human bre	Aai34661 Probe #33	Aba55007 Human foe	Aai13308 Probe #32		Abt14895 Pathogen	Aax24906 Mouse elo	Acn44341 Mouse mRN	Adq79072 Novel can	Aal41031 DNA encod	Aac85836 Nucleotid	Aac75801 Human ORF	Adb49166 Novel hum	Adq99406 DNA encod	Aai59183 Human pol	æ	Aac77686 Human can	Aaz77530 Human ova	Acn38837 Tumour-as	Adr25399 Breast ca	Adf81412 Leukaemia	Abk83658 Human cDN	Adc37617 Human nuc

ALIGNMENTS

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RESULT 1
AAC64967
ID AAC6
XX AAC6
XX Pig
XX Pig
XX Pig
XX Pig
XX Pig
XX Pig
XX Brod
XX Sus
XX GB23
XX GB23
XX GB23
XX I5-A
PR 15-A
PR 
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15-APR-1999;
01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pig; sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling; cardiac hypertrophy; heart failure; hypertension; Darier-White dise. Brodys disease; diabetes; ss.
                                                                                                                                                                                                                              Disclosure; Fig 11; 108pp; English.
                                                                                                                                                                                                                                                                                                                                               Identifying modulators of sarco/endoplasmic reticulum calcium ATPase, useful potentially for treating disorders of calcium homeostasis, e.g. \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB2349217-A.
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99US-0129596P.
99GB-00012736.
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ova

The present invention is concerned with methods of using C. elegans identify compounds which are capable of up- and down-regulating the activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). protein is involved in cell signalling, and elevated levels affect cellular processes such as contraction, secretion and cell cycling.

This ដ

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RESULT 2
ADB53082
ID 53082
ID 53082
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AC ADB5
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19-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-APR-2002;
10-APR-2002;
10-APR-2002;
                                                                                                                                                                               Mendrick
Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxicity marker; to
                                                         identifying hepatoto profile of a tissue
                                                                                Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene express
                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-2002;
11-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2002;
13-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                                                                                2002US-0373601P
2002US-0373602P
2002US-0374139P
2002US-0378370P
2002US-0378652P
2002US-0378655P
2002US-0378658
2002US-0378658
2002US-03942530P
2002US-03942530P
2002US-03942530P
2002US-0394250P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2002US-0353171P.
; 2002US-0363534P.
; 2002US-0370248P.
; 2002US-0371134P.
; 2002US-0371135P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   t; gene expression profile; heparker; toxicity progression; drug hepatocyte toxicity modelling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be used to it pathologies,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 45
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2002US-0371413P.
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                                                                                                                                                                                                 Porter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diabetes, Darier-White disease and
                                                                                                                                                                                                                                          INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to identify compounds for use in the treatment gies, cardiac hypertrophy, heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; 41 C;
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                                                           cell sample
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                                                                                                                                                                                                   Johnson
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                                                         sample
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Pred. No. 3.
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                                                         comprises
to a datab
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ing; gene; ds.
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                                                                                                                                                                                                   Castle
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                                                         Tox mean and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
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                                                                                expression
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Matches
                                          Query Match
                                                                                                                                              The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or call. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte covicity and office of the present in progression or for the present sequence represents a primary rat hepatocyte covicity.
                                                                                     Sequence
                                                                                                                                   toxicity
                        Local
                                                                                                                          screening. The present
city modelling related
  l Similarity
70; Conser
                                                                                        701
46.5%;
nilarity 68.0%;
Conservative
                                                                                     BP;
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                                                                                                                                   gene sequence from the present invention
    0,
                        Score 50.2;
Pred. No. 8
    Mismatches
                      8.1e-06
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                   TCTCATCTGCCTCCTGCTGATTTGCATTATCGTCATGCTCCTG 108
CTTGATATGTCTGCTGCTGATATGCATCATTGTGATGCTTCTG 329
                                                                            TGAAATGCCCCAGCAAGCGCGTCAGAACCTCCAGAACCTCTTTATCAATTTCTGTCTCAT 286
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TGAGAGAAGGCCTCAGGCCAGGAACCTCCAGAATGCTTTCATTGCTTTTTGTCTGAT

65

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RESULT 3
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IID ADR97285
AC ADR9
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XX ADR9
XX Huma
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XX US20
XX J0-S
PD 30-S
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22-OCT-2002; KRAN/) KRANIAS E G. HAGHIGHI K. 2002US-0420295P

Phospholamban polymorphism assessment in individual, for determining for developing cardiovascular disease, by comparing analysis of the nucleotide fragment with a predetermined phospholamban nucleotide Claim 15; SEQ ID NO ļ 15pp; English risk

WPI; 2004-689841/67

Kranias

, EG,

Haghighi

(HAGH/)

The invention relates to a method of phospholamban polymorphism assessment in an individual which comprises comparing the analysis nucleotide fragment with a predetermined phospholamban nucleotide fragment to determine whether the individual carries a phospholamban polymorphism. The methods and phospholamban polymorphism. are useful for determining an polymorphism the

Claim 44; SEQ ID

NO 3624; 874pp; English

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Result
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen
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      UI-R-CSO-
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8 892817 MA
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ALIGNMENTS

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 381)
Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S., Soares,M., Bonaldo,F. and Hatey,F. Email: tosser@toulouse.inra.fr Sequence cleaned of vector, adapt at sigenasupport@jouy.inra.fr to Contact: Tosser-Klopp G Genetique Animale Institut National de la Recherche Chemin de Borde-Rouge - Auzeville A Pig Normalised Multi-Tissue cDNA Library Unpublished (2003) Sus scrofa (pig) Sus scrofa BX669692 Sus Scrofa library (scac) Sus scrofa cDNA clone Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08 scac0028i.c.02 5prim, Plate: 0028 row: c BX669692.1 GI:37979481 /organisme"Sus scrofa"
/organisme"Sus scrofa"
/mol_type="mRNA"
/db xref="taxon:9823"
/clone="scac0028i.c.02"
/tissue_type="mixed"
/clone Tib="Sus Scrofa library (scac)"
/clone Tib="Sus Scrofa library (scac)"
/clone Tib="Sus Scrofa library tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pitultary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder" FRANCE ocation/Qualifiers column: 2. mRNA sequence. 381 bp adaptator and repetitions. Contact unity to obtain the chromatogram of this Agronomique BP27, 31326 mRNA linear Castanet-Tolosan Euteleostomi; Sus. EST 07-MAY-2004 Contact us

47.0%;

Score 50.8;

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Length 381;

EST 07-MAY-2004

Sus.

Euteleostomi;

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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
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Institut National de la Recherche
Chemin de Borde-Rouge - Auzeville
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1 (bases 1 to 702)

Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S., Soares, M., Bonaldo, F. and Hatey, F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="scan0013d.j.1.4"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/dev_stage="from embryos to stain, kidney, liver,
/note="tissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo uretral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"
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/mol_type="mRNA"
/db_xref="taxon:9823"
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0; Mismatches
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Pred. No. 0.00013;
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Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C.,
Soares, M., Bonaldo, F. and Hatey, F.
A Pig Normalised Multi-Tissue CDNA Library
Unpublished (2003)
                                                                                                           Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa;
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Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EX674983 Type 1 124 bp 1 125 pp 1 125 p
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Soares, M.,
                          Bonnet, A.,
                                                       1 (bases 1 to 740)
                                                                                                                                                                                                                         BX924154.1 GI:41141002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Tosser-Klopp G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa (pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX674983.1 GI:38008935
                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTAATATGCCTCTTGCTGATTTGCATCATCGTGATGCTTCT
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/mol type="mRNA"

/db xref="taxon:9823"

/clone="scac0039i.h.23"

/tissue type="mixed"

/clone Tib="Sus Scrofa library (scac)"

/clone="vector: pT771D-pac vector; tissues: adipose tissue,
/note="vector: pT771D-pac vector; tissues: heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo uretral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0039,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                    Eutheria;
  Bonaldo, F.
                             Tosser-Klopp, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.0%;
68.6%;
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                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>,</u>
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                                                                                                                                                                                                                                                                             mRNA sequence.
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  and Hatey, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                          740 bp
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EST 07-MAY-2004

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Gaps

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Result
No.
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Maximum DB
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Perfect score:
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Maximum Match 10
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30.4
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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

3: /cgn2_6/ptodata/1.

4: /cgn2_6/ptodata/1.

5: /cgn2_6/ptodata/1.

6: /cgn2_6/ptodata/1.
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Gapop 10.0 , Gapext 1.0
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47.0
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Listing first 45 summaries
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
   7, 2005, 09:02:25 ; Search time 61.7778 Seconds (without alignments) 2860.541 Million cell updates/sec
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US-09-513-399C-10799
US-09-913-13-99C-10799
US-09-949-016-13181
US-09-949-016-15336
US-09-949-016-15336
US-09-188-930-28
US-09-188-930-28
US-09-188-930-203
US-09-188-930-203
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US-09-312-283C-203
US-09-949-016-17088
US-09-949-016-17088
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              Sequence 9, Appli
Sequence 13, Appl
Sequence 10799, Ap
Sequence 1139, Ap
Sequence 26, Appl
Sequence 26, Appli
Sequence 1076, Ap
Sequence 1161, Ap
Sequence 203, Appli
Sequence 203, Appli
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Sequence 5041, Appli
Sequence 11, Appli
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Sequence 11, Appli
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 11, Appl
999, App
999, Appl
4, Appli
17088, A
12426, A
202802,
17449, A
10, Appl
RESULT 2
US-09-549-872B-13
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERBNCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
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	SSIU, A	17610, 1	14139, 4	3, Appli	12378, 1	17304, F	636, App	5562, Ap	27, Appl	160, App	3036, Ap	11, Appl	1, Appli	82861, A	492, App	2272, Ag	35, Appl	and sea

GENERAL INFORMATION: APPLICANT: Zwaal, Richard APPLICANT: Zwaal, Richard APPLICANT: Groenen, Jose APPLICANT: Groenen, Jose TITLE OF INVENTION: COMPOUND SCREENING METHODS FILE REFERENCE: D00590/70008 (JRV/RE) CURRENT APPLICATION NUMBER: US/09/549,872B CURRENT FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: GB 9908670.4 PRIOR FILING DATE: 1999-04-15 PRIOR APPLICATION NUMBER: US 60/129,596 PRIOR APPLICATION NUMBER: GB 9912736.7 PRIOR FILING DATE: 1999-06-01 NUMBER OF SEQ ID NOS: 39 SOFTWARE: PATENTING DATE: 1999-06-01 NUMBER OF SEQ ID NOS: 39 SOFTWARE: PATENTING DATE: 1999-06-01 SEQ ID NO 9 ; LENGTH: 159 ; TYPE: DNA ; ORGANISM: Sus sp. US-09-549-872B-9 RESULT 1 US-09-549-872B-9 Query Match Best Local Similarity Matches 70; Conserv Sequence 9, Application Patent No. 6540996 114 CTTAATATGCCTCTTGCTGATTTGCATCATCGTGATGCTTCT 155 99 54 TCTCATCTGCCTCCTGCTGATTTGCATTATCGTCATGCTCCT 107 TGAGAGAAGGCCTCAGGCCAGGAAACCTCCAGAATGCTTTTCATTTGTCTGAT TGANATGCCTCAACAAGCACGTCAAAACCTTCAGAACCTATTTATCAATTTCTGTCTCAT Conservative 47.0%; US/09549872B 0; Score 50.8; DB 4; Pred. No. 5.6e-08; 0; Mismatches 32 4. Length 159; Indels

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Gaps

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US-09-949-016-1439
, Sequence 1439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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                                                                                      RESULT 4
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PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 13
LENGTH: 159
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/122,487 PRIOR FILING DATE: 1999-02-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                 Local
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Local Similarity 68.6%;
                                                                                                                                          309
                                                                                                                                                                                                           249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 CTTAATATGCCTCTTGCTGATTTGCATCATCGTGATGCTTCT 155
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67; Conserv
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                                                                                                                                          CTTAATATGTCTCTTGCTGATCTGTATCATCGTGATGCTTCT 350
                                                                                                                                                                                                             rgaaatgccrcaacaagcacgrcaaaagcracagaatcrarrarcaarricigicicar
                                                                                                                                                                                                                                           TGAGAGAAGGCCTCAGGCCAGGAACCTCCAGAATGCTTTCATTGCTTTTTGTCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAAATGCCTCAACAAGCACGTCAAAACCTTCAGAACCTATTTATCAATTTCTGTCTCAT 113
                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description of Artificial Sequence:HUMANIZED PLB cDNA
                                                                                                                                                                                                                                                                                               42.6%;
                                                                                                                                                                                                                                                                             Score 46; DB of Pred. No. 4e-0000; Mismatches
                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
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Pred. No. 5.6e-08;
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                                                                                                                                                                                                                                                                                                 4e-06;
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                                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                              Length 480;
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; ORGANISM: Human
US-09-949-016-13181
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US-09-949-016-1439
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13181
LENGTH: 16062
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13181, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1439
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION. WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                         Local Similarity
nes 67; Conserv
                                                                                    12661 TGAAATGCCTCAACAAGCACGTCAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCAT 12720
12721 CTTAATATGTCTCTTGCTGATCTGTATCATCGTGATGCTTCT 12762
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Pred. No. 6.7e-06;
0; Mismatches 35
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Pred. No. 1.7e-05;
D; Mismatches 35;
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OF DETECTION AND USES THEREOF
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US-09-124-671-26 ; Sequence 26, Application US/09124671A

RESULT 6

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Maximum DB seq length: 2000000000
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Perfect score:
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/ Cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USOA_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USOA_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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US-10-724-532-4

US-10-724-532-6

US-10-724-532-6

US-10-371-101-9

US-10-371-101-13

US-10-691-412-1
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Sequence 3, 1
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ALIGNMENTS

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FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOPTWARE: Patentin version 3.2
SEQ ID NO 3
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US-10-724-532-3
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Publication No. US20040203027A1
GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
                                                                                                                          Query Match 100.0%; Score 108; DB 20; Best Local Similarity 100.0%; Pred. No. 1.3e-26; Matches 108; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: mus musculus
                                                                                                                                                                                                                                                                               ENGTH: 108
  61 CTGATTCTCATCTGCCTCCTGCTGATTTGCATTATCGTCATGCTCCTG 108
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                                                                  ATGCATGAGAGAAGGCCTCAGGCCAGGCAGAACCTCCAGAATGCTTTCATTGCTTTTTTGT
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; ORGANISM: mus musculus
US-10-724-532-5
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US-10-724-532-5
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TYPE: DNA
ORGANISM: mus musculus
US-10-724-532-4
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Publication No. US20040203027A1
GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic TITLE OF INVENTION: Reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10724532 Publication No. US20040203027A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              SEQ ID NO 5
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                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
ETILE REPERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR PILING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                            ENGTH: 135
                                                                                                                                                                           Local Similarity
                                                                                                                                                       108; Conservative
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Pred. No. 1.4e-26;
; Mismatches 0;
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RESULT 4

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; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus s
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; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6
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CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR PPLICATION NUMBER: GB 9912736.7
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR APPLICATION NUMBER: 09/549,872
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PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035.US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
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Publication No. US20040203027A1
                                                                                                                                                                       Matches
                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/10371101 Publication No. US20030149995A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 108; Conservative
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CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 CTTAATATGCCTCTTGCTGATTTGCATCATCGTGATGCTTCT
                        66 TCTCATCTGCCTCCTGCTGATTTTGCATTATCGTCATGCTCCT 107
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                                                                                  54 TGANATGCCTCANCANGCACGTCANANCCTTCAGAACCTATTTATCAATTTCTGTCTCAT 113
                                                                                                                                                                       70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGCATGAGAGAAGGCCTCAGGCCAGGCAGAACCTCCAGAATGCTTTCATTGCTTTTTGT 60
                                                                                                                          6 TGAGAGAAGGCCTCAGGCCAGGCAGAACCTCCAGAATGCTTTCATTGCTTTTTTGTCTGAT 65
                                                                                                                                                                       Conservative
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68.6%;
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                                                                                                                                                                    Score 50.8; DB 1
Pred. No. 3.8e-07
0; Mismatches 3
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Pred. No. 1.4e-26;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 July 7, 2005, 09:02:25; Search time 999.333 Seconds (without alignments) 5236.654 Million cell updates/sec
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108
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Score Match Length	Length	- 5	ID	Description
52.4 48.5	828	4.	RABPHLAM2	M63601 Rabbit phos
	2841	4	OCPHLAM	Y00761 O.cuniculus
8 47.0	159	0	BD247907	BD247907 Method fo
8 47.0	159	δ	BD247911	BD247911 Method fo
8 47.0	159	σ	AR302003	AR302003 Sequence
8 47.0	159	σ	AR302007	AR302007 Sequence
8 47.0	159	o	AX040487	AX040487 Sequence
8 47.0	159	0	AX040491	AX040491 Sequence
8 47.0	737	4.	SSPLB	X15075 Pig mRNA fo
2 46.5	159	10	S95853	S95853 phospholamb
2 46.5	386	10	S95849	S95849 Rattus sp.
2 46.5	701	10	RNPHLAMB	X71068 R.norvegicu
2 46.5	1786	10	RATPHOLA02	L03382 Rat phospho
2 46.5	223728	N	AC097906	AC097906 Rattus no
2 46.5	231910	N	AC128365	AC128365 Rattus n
	130240	S	BX276081	BX276081 Zebrafish
6 44.1	648	10	BC061097	BC061097 Mus muscu
6 44.1 7 43.5	940	10	S46792	S46792 phospholamb
6 44.1 7 43.5 7 43.5		J	AC100317	AC100317 Mus muscu
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30.4	30.4	30.4	30.7	33.3	40.4	41.1	41.1		41.1	42.6		42.6	42.6		42.6	42.6		42.6	42.6	42.6	42.6	43.0	43.0	43.3	43.5
2254	1893	1593	204114	147419	315	2614	832	832	314	150290	66092	60797	1691	1635	1635	1635	980	480	480	323		3423	3312	133901	177018
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AK125620	HSHR21SPA	AK098521	AC108810	HS738P11	AR121629	CFPHLX	DOGPLBA	DOGPHL	AY514751	HS509L4	AL136974	AL355356	BC005269	HUMPHLAM	AX329653	CQ718671	HSPLBG2	BD030469	AX894936	HUMPLAM	CQ447405	CHKPLB2	CHKPLB	BX537355	AC099716
AK125620 Homo	X98294 Homo sapien	AK098521	AC108810	AL031736	AR121629	Y00399	M35393	M16012	AY514751 Canis fam	299496 Human DNA	AL136974	AL355356	BC005269	M63603 Human phos	AX329653	CQ718671	AF177764	BD030469	AX894936	M60411 Human phosp	CQ447405 Sequence	M59038	M59039	BX537355	AC099716

ALIGNMENTS

ORIGIN	CDS	exon		source	FEATURES	COMMENT	MEDLINE	JOURNAL	TITLE	AUTHORS	REFERENCE	ORGANISM	SOURCE	SEGMENT	VERSION	DEFINITION	RESULT 1 RABPHLAM2/c
EMPQQARQNLQNLI	2	Join(moseuv.i:855. 343,426. 859) /product="phospholamban" 428. 858	/organism="Oryccolagus cuniculus" /mol_type="genomic DNA" /db_xref="taxon:9986" /tisus_lib="rabbit genomic" /tisus_lib="rabbit genomic"			1828805 Original source text: Rabbit DNA.	91268032	cDNA, and assignment of the gene to human chromosome 6 J . Biol. Chem. 266 (18), 11669-11675 (1991)	MacLennan,D.H. Structure of the rabbit phospholamban gene, cloning of the human	Fujii, J., Zarain-Herzberg, A., Willard, H.F., Tada, M. and		Oryctolagus cuniculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Oryctolagus cuniculus (rabbit)	pnospnoiamban. 2 of 3	M63601.1 GI:165636	858 pp DNA linear אמיי בייבור אמייבור אמייבור בייבור בייבור בייבור בייבור בייבור בייבור בייבור אמייבור בייבור בייבור בייבור בייבור בייבור בייבור בייב אמייבור בייבור בי	

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Best Local :
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                                                       159 bp
Method for screening compounds.
BD247907
BD247907.1 GI:33057677
JP 2002541859-A/9.
                                    Sus sp.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 159)
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 2841)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O.cuniculus mRNA for Y00761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2962883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phospholamban gene
FEBS Lett. 227 (1),
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                                                                                                                                                                                                                                                     AGGAGCATGACGATAATGCAAATCAGCAGGAGGAGGAGATGAGAATCAGACAAAAAAGCAATG
                                                                                                                                                                                   AATAGGTTCTGGAGGTTTTGACGTGCTTGTTGAGGCATTTCA 231
                                                                                                                                                                                                AAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA 103
                                                                                                                                                                                                                                      AGAAGCATGACGATGATGCAGATCAGCAGGAGACATATCAAGATGAGACAGAAATTGATA
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                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lett.
                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="phospholamban"
/protein_id="CAA68730.1"
/db_xref="GI:1662"
/db_xref="GA:270006"
/db_xref="GA:270006"
/db_xref="GA:270006"
/translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryctolagus cuniculus"
/mol_type="mRNA"
/db_xref="taxon:9986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                   48.5%;
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            Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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phospholamban.
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Pred. No. 2.2e-06;
0; Mismatches 31;
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TITLE
Query Match
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Matches 70; Conserv
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Best Local Similarity
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Method for screening compounds

Patent: JP 2002541859-A 9 10-DEC-2002;

DEVGEN NV

OS Sus sp. (pig)
PN JP 2002541859-A/9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PF 14-APR-2000 JP 2000612503
PF 15-APR-1999 GB 9908670.4,15-APR-1999 US
01-UN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C1201/42,C12N15/09,C1201/02,C12N15/00
CC Method for screening compounds
CC Method for screening compounds
FH Key 1. 159
FT source 1. 159
FT source 1. 159
FT source (pig)'.
                                                                                                                                                                      Method for screening compounds

Patent: JP 2002541859-A 13 10-DEC-2002;

DEVGEN NV
OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PF 14-APR-2000 JP 2000612503
PF 15-APR-1999 GB 9908670.4,15-APR-1999 US 60
PR 15-APR-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C1201/42,C12N15/09,C1201/02,C12N15/00
CC Description of Artificial Sequence: HUMANIZED PIC
Key Location/Qualifiers
FT source /organism='Artificial Sequence'
PT source /organism='Artificial Sequence'
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Method for screening compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Zwaal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other sequences;
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al,R., Groenen,J. and Bogaert,T.
47.0%;
nilarity 68.6%;
Conservative
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                                                                                                                                                     /organism='Artificial
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/mol_type="genomic DNA"
/db_xref="taxon:9826"
                                                                                    organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Score 50.8; D
Pred. No. 6e-0
0; Mismatches
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                   8; DB 6e-06;
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1: geneseqn1980s:*

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length: 2000000000
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Match
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Gapop 10.0 , Gapext 1.0
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108
caggagcatgacgataatgc....tgaggccttctctcatgcat
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Length
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                       ABN22344
AACH66724
ACH16833
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ADN04087
ADP21384
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ADP07907
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     Aac64967 Pig phosp
Adb53082 Primary r
Adr97285 Human ORP
Abn22344 Human ORP
Aac06724 Human ORP
Aac06724 Human acu
Abl61825 Colon ade
Adn04087 Antipsori
Adp21184 Gene PLN
Ach16738 Human acu
Ach16738 Human acu
Ach18023 Human acu
Ach18023 Human acu
Ach1805 Human acu
Ach16630 Human acu
Ach16630 Human acu
Ach16630 Human acu
Ach16630 Human col
Ach30165 Human col
Ach30165 Human col
Ach30165 Human col
Ach301907907 Human CN
Abg60633 Human col
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4.5	44	43	42	41	40	39	38	37	36	35	34	ω G	32	31	30	29	28	27	c 26	25	24	23	22	21	
30	30	30	30	30	30	30.2	30.2	30.4	30.4	31.2	32	32	32	32	32	32	32.8	٠	•	32.8	٠	•	•	32.8	
27.8	27.8	27.8	27.8	27.8	27.8	28.0	28.0	28.1	28.1	28.9	29.6	29.6	29.6	29.6	29.6		30.4			30.4		30.4		30.4	
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AAK28730	ABA24770	ABA44562	AAI34661	ABA55007	AAI13308	ACF73801	ABT14895	AAX24906	ACN44341	ADQ79072	AAL41031	AAC85836	AAC75801	ADB49166	ADQ99406	AAI59183	ADQ21778	AAC77686	AAZ77530	ACN38837	ADR25399	ADF81412	ABK83658	ADC37617	
Aak28730 Human bon	Probe	Aba44562 Human bre	Aai34661 Probe #33	Human	Aai13308 Probe #32	Acf73801 Staphyloc	Abt14895 Pathogen	Aax24906 Mouse elo	Acn44341 Mouse mRN	Adq79072 Novel can	Aal41031 DNA encod	Aac85836 Nucleotid	Aac75801 Human ORF		Adq99406 DNA encod	Aai59183 Human pol	Adq21778 Human sof	Aac77686 Human can	Aaz77530 Human ova	Acn38837 Tumour-as	Adr25399 Breast ca	Adf81412 Leukaemia	Abk83658 Human cDN	Adc37617 Human nuc	

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RESULT 1
ARC64967/c
ID ARC649
XX ARC649
XX Pig; B
XX Pig
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15-APR-1999;
01-JUN-1999;
                                                                                                                                                                                                                                                                                   Identifying modulators of sarco/endoplasmic reticulum calcium ATPase, useful potentially for treating disorders of calcium homeostasis, e.g cardiac hypertrophy.
                                                                                                                                                                                                            Disclosure; Fig 11; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-658082/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pig; sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling;
cardiac hypertrophy; heart failure; hypertension; Darier-White disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC64967 standard;
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99US-0129596P.
99GB-00012736.
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The present invention is concerned with methods of using C. elegans identify compounds which are capable of up- and down-regulating the activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). protein is involved in cell signalling, and elevated levels affect cellular processes such as contraction, secretion and cell cycling.

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Best Local (
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13-MAR-2002;
08-APR-2002;
10-APR-2002;
10-APR-2002;
11-APR-2002;
11-APR-2002;
11-APR-2002;
11-APR-2002;
12-APR-2002;
22-APR-2002;
08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
                                                                                                Mendrick
Elashoff
                  mean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methods can be used to identify compounds for use in the treatment some muscle pathologies, cardiac hypertrophy, heart failure,
                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                             Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene express. profile of a tissue or cell sample to a database of Tox mean and non-
                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         primary
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primary rat hepatocyte toxicity modelling; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primary rat hepatocyte toxicity modelling related gene
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                  values.
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                                                                                                                                                   2002US-0353171P.
2002US-0370248F.
2002US-0371134P.
2002US-0371135P.
2002US-0371150P.
2002US-0371150P.
2002US-0371419P.
2002US-0374119P.
2002US-037419P.
2002US-0378652P.
2002US-0378652P.
2002US-0378655P.
2002US-0378659.
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                                                                                                          Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   athologies, cardiac hypertrophy, heart failure, diabetes, Darier-White disease and Brodys disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression profile; hepatotoxicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45
                                                                                                                                INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
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68.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       701
                                                                                                          Johnson
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 T; 0 U; 0
                              comprises comparing a gene expression to a database of Tox mean and non-Tox
                                                                                                         Higgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug screening;
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Claim 44; SEQ ID

NO 3624; 874pp; English

The invention relates to a method of phospholamban polymorphism assessment in an individual which comprises comparing the analysis nucleotide fragment with a predetermined phospholamban nucleotide fragment sequence to determine whether the individual carries a phospholamban polymorphism. The methods and phospholamban polymorphism.

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polymorphism

are

for

determining

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Claim

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ID NO

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English

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RESULT 3
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ID ADR97285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                               Phospholamban polymorphism assessment in individual, for determining for developing cardiovascular disease, by comparing analysis of the nucleotide fragment with a predetermined phospholamban nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                               US2004191802-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human phospholamban polymorphism fragment
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ORIGIN SOURCE ORGANISM RESULT 1 BX669692/c FEATURES REFERENCE COMMENT DEFINITION KEYWORDS ACCESSION VERSION TITLE JOURNAL AUTHORS source Unpublished (2007)
Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Institut National de la Recherche BP27, 31326 Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 381)
Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S., Soares, M., Bonaldo, F., and Hatey, F. A Pig Normalised Multi-Tissue cDNA Library Unpublished (2003) Sus scrofa (pig) Sus scrofa BX669692 Sus Scrofa library Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08 BX669692.1 GI:37979481 BX669692 scac0028i.c.02 5prim, mRNA sequence. /organism="Sus scrofa"
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/db_xref="taxon:9823"
/clone="scac0028i.c.02"
/clone="scac028i.c.02"
/clone="scac028i.c. 0028 row: c 28 row: c column: 2. ocation/Qualifiers 381 bp (scac) Sus scrofa cDNA clone m.RNA linear Castanet-Tolosan Euteleostomi; Sus. EST 07-MAY-2004

Query Match

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Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
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Institut National de la Recherche
Chemin de Borde-Rouge - Auzeville
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Unpublished (2003)
Contact: Tosser-Klopp G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 702)

Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villeger,S.,
Soares,M., Bonaldo,F. and Hatey,F.
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
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/clone lib="Gus Scrofa library (scan)"
/clone="tissues: adipose tissue, brain, kidney, liver,
/note="tissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo uretral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"
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/clone="scan0013d.j.14"
/tissue_type="mixed"
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                REFERENCE
                                                                                                                                    ACCESSION
                                                                                                                                                                      DEFINITION
                                                                                                    KEYWORDS
                                                                                                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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AUTHORS
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RESULT 3

BX924154 Sus Scrofa library (scan) S scan0011d.f.23 5prim, mRNA sequence.

740 bp

mRNA

Sus scrofa cDNA clone

EST 07-MAY-2004

BX924154

BX924154.1

GI:41141002

BX924154

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 740)

Tosser-Klopp,G., Benne,F., Bonaldo,F. and Hatey,F.

Cabau, C.,

Euteleostomi; Sus.

Bonnet, A., Soares, M., Sus scrofa (pig)

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Query Match
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Fax: 33 (0) 5.61.28.53.08

Email: tosser@toulouse.inra.fr

Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
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Soares,M., Bonaldo,F. and Hatey,F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 724)
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                                                                             AAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA 103
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AATAGGTTCTGAAGGTTTTGACGTGCTTGTTGAGGCATTTCA
                                                                                                                                                                   AGAAGCATCACGATGATGCAAATCAGCAAGAGGCATATTAAGATGAGACAGAAATTGATA 279
                                                                                                                                                                                                                                                                                                                                  Conservative
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/db xref="taxon:9823"

/clone="scac0039i.h.23"

/clone="scac0039i.h.23"

/tissue type="mixed"

/clone lib="Sus Scrofa library (scac)"

/clone lib="Sus Corofa library (scac)"

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Auzeville
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BP27, 31326
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Issued_Patents NA:*

1: /cgn2_6/ptodata/1/1na/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/1na/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/1na/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/1na/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/1na/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/1na/backfiles1.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                    7, 2005, 09:02:25 ; Search time 61.7778 Seconds (without alignments) 2860.541 Million cell updates/sec
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US-09-513-99C-110799
US-09-913-13-99C-1161
US-09-949-016-13181
US-09-949-016-13181
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US-09-312-283C-293
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US-09-
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               Sequence 9, Appli sequence 113, Appl sequence 113181, Appl sequence 11439, Appl sequence 26, Appl sequence 1161, Appl sequence 1161, Appl sequence 213, Appl sequence 203, Appl sequence 203, Appl sequence 5041, Appl sequence 5041, Appl sequence 11578, App sequence 11, Appl sequence 12426, A sequence 12426, A sequence 12426, A sequence 11449, A sequence 
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APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 60/549,872B
CURRENT FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR SEQ ID NOS: 39
SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
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US-09-270-767-5510 ALIGNMENTS	US-09-949-016-17610	US-09-949-016-14139	US-09-820-007-3	US-09-949-016-12378	US-09-949-016-17304	US-09-949-016-636	US-09-949-016-5562	US-09-774-528-27	US-09-149-476-160	US-09-949-016-3036	US-09-552-225A-11	US-08-309-182B-1	US-09-949-016-82861	US-09-107-433-492	US-09-583-110-2272	US-09-949-001-35	US-09-949-001-29
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9
                                                                                                             RESULT 2
US-09-549-872B-13/c
US-09-549-872B-13/c
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
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Best Local Similarity
Matches 70; Conserv
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
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Pred. No. 5.6e-08;
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CURRENT FILING DATE:

2000-04-14

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US-09-949-016-1439/c
Sequence 1439, Application
Patent No. 6812339
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-513-999C-10799
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PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10799, Ap
Patent No. 6783961
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Best Local (
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Best Local (
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CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 59.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 480
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Local Similarity 68.6%;
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 VENTER, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description of Artificial Sequence:HUMANIZED PLB cDNA
                                                                                                                                                                                                                                                                                      42.6%;
Craig et al
                                                  US/09949016
                                                                                                                                                                                                                                                                                      Score 46;
Pred. No.
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                                                                                                                                                                                                                                                                        Mismatches
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Thes 35; Indels
                                                                                                                                                                                                                                                                                                     DB 4;
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                                                                                                                                                                                                                                                                                                       Length 480;
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; ORGANISM: Human
US-09-949-016-1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: CL001107
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13181, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                SEQ ID NO 13181
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LENGTH: 1635
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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ITTLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS

FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                 Local Similarity 65.7
les 67; Conservative
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12702
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  AATAGATTCTGTAGCTTTTGACGTGCTTGTTGAGGCATTTCA
                                          AAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA 103
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65.7%;
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Pred. No. 1.7e-05;
0; Mismatches 35
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OF DETECTION AND USES THEREOF
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RESULT 6 US-09-124-671-26/c ; Sequence 26, Application US/09124671A

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications Ni / cgn2 6/ptodata/1/pubj 2: / cgn2 6/ptodata/1/pubj 3: / cgn2 6/ptodata/1/pubj 3: / cgn2 6/ptodata/1/pubj 5: / cgn2 6/ptodata/1/pubj 6: / cgn2 6/ptodata/1/pubj 6: / cgn2 6/ptodata/1/pubj 6: / cgn2 6/ptodata/1/pubj 9: / cgn2 6/ptodata/1/pubj 9: / cgn2 6/ptodata/1/pubj 9: / cgn2 6/ptodata/1/pubj 10: / cgn2 6/ptodata/1/pubj 10: / cgn2 6/ptodata/1/pubj 11: / cgn2 6/ptoda
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Gapop 10.0 , Gapext 1.0
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: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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SUMMARIES
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42.6	47.0	47.0	100.0	100.0	100.0	100.0	Query
159	159	159	135	135	108	108	Query Match Length DB
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US-10-691-412-1	US-10-371-101-13	US-10-371-101-9	US-10-724-532-6	US-10-724-532-5	US-10-724-532-4	US-10-724-5	ID
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605	CCTTC2	251199	113306	1137	1269	415	639	2175	2175	1938	613	2220	2180	10625	10625	10625	6481	6481	3925	3748	3647	3647	3647	2419	1896	652	492	407	315	315	315	487	394	418	380	1635	1635	,
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US-10-027-632-238890	-TO-704-073	-10-482-029-205	-10-292-798-100	437-963-886	-10	US-09-864-761-3236	ш	US-09-832-292-7	US-09-994-485-3	US-10-087-192-740	US-10-767-701-25701	US-10-425-115-167740	US-10-425-114-557	US-10-690-276-3	US-10-023-219-3	US-09-727-384-5	US-10-117-722-1076	US-10-037-270-1076	US-10-723-860-4598	US-09-925-301-80	-10-848-755A-14	-10-342-887-126	-10-	-09-81	-10-72	6	-09-91	-09-91	-10-873-594-2	-10-877-930-2	-10-815-514-2	US-09-918-995-5377	-995-421	US-09-918-995-5235	-995-395	US-10-843-641A-162	-09-873-367C-16	
2388	educate von'	205.		Sequence 88641, A	e 1475,	Sequence 3236, Ap	e 4			Sequence 740, App	æ				e		1	1076,	4598,	80, AE	148, /	1260,	e			434	Œ	3847	26,	26,	e 26,	5377	ø	e 5235	e 3950	e 162, /	e 162,	

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                                                                                                                                                                                                                                                                       ; TYPE: DNA; mus musculus; ORGANISM: mus musculus US-10-724-532-3
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US-10-724-532-3/c
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo) plasmic TITLE OF INVENTION: Reticulum FILE REFERENCE: SR RPA CURRENT APPLICATION NUMBER: US/10/724,532 CURRENT APPLICATION NUMBER: US/10/724,532 CURRENT FILING DATE: 2003-11-29 PRIOR APPLICATION NUMBER: US 60/430322 PRIOR APPLICATION NUMBER: US 60/430322 PRIOR PILING DATE: 2002-12-02 NUMBER OF SEQ ID NOS: 6 SOPTWARE: Patentin version 3.2 SEQ ID NO 3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10724532
Publication No. US20040203027A1
GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
                                                                                                                                                           Query Match 100.0%; Score 108; DB 20; Best Local Similarity 100.0%; Pred. No. 1.3e-26; Matches 108; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 108
                                                        108 CAGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAATCAGACAAAAAGCAAT 49
  61 GAMAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCATGCAT 108
                                                                                  1 CAGGAGCATGACGATAATGCAAATCAGCAGGAGGAGGAGATGAGAATCAGACAAAAAGCAAT 60
                                                                                                                                                                 Indels
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; TYPE: DNA; mus musculus US-10-724-532-5
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US-10-724-532-4
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US-10-724-532-5/c
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; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4
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Publication No. US20040203027A1

GENERAL INFORMATION:

APPLICANT: Reed, Thomas D

TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo) plasmic TITLE OF INVENTION: Reticulum

FILE REFERENCE: SR RPA

CURRENT PILING DATE: 2003-11-29

PRIOR APPLICATION NUMBER: US/10/724,532

CURRENT FILING DATE: 2002-12-02

PRIOR FILING DATE: 2002-12-02

NUMBER OF SEQ ID NOS: 6
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Publication No. US20040203027A1
GENERAL INFORWATION:
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 135
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Best Local Similarity
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GAAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCATGCAT 13
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100.0%; Pred. No. 1.4e-26;
Mismatches 0;
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APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
APPLICANT: Bogaert, Thierry
APPLICATION COMPOUND SCREENING METH
FILLE REFERENCE: D00590,70035.US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILLING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILLING DATE: 1999-04-15
PRIOR FILLING DATE: 1999-04-15
PRIOR FILLING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: GB 9912736.7
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US-10-371-101-9/c
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Publication No. US20040203027A1
GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo) plasmic TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION UNMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
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Best Local Similarity 100.0%;
Matches 108; Conservative 0
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                                                                                                                                                                 Matches
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PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
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                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                          TYPE: DNA
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Pred. No. 3.8e-07;
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Pred. No. 1.4e-26;
Mismatches 0;
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AC100317 Mus muscu AC099716 Mus muscu M59039 Chicken car M59038 Chicken pho CQ447405 Sequence M60411 Human phosp

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          AX040491 Sequence
X15075 Pig mRNA fo
S95833 phospholamb
S95849 Rattus sp.
X71068 R. norvegicu
L03382 Rat phospho
AC097996 Rattus no
AC128365 Rattus no
BX276081 Zebrafish
BX537355 Zebrafish
BC061097 Mus muscu
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700761 O.cuniculus

BD247907 Method fo

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                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                 Original source text: Rabbit DNA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 858)
Fujii,J., Zarain-Herzberg,A., Willard,H.F.,
MacLennan,D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phospholamban.
2 of 3
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/protein_id="AAA31445.1"
/db_xref="GI:165639"
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                                                                                                /function="regulatory
Ca-ATPase"
                                                                                                                                                                             mol_type="genomic DNA"
/db_xref="taxon:9986"
/tissue_lib="rabbit genomic"
join(M63600.1:855. .943,428. .858)
/product="phospholamban"
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CHKPLB
CHA936
CQ447405
HUMPLAM
AX894936
BD030469
HSPLBG2
CQ71867
AU329653
HUMPHLAM
BC005269
AL136974
HS509L4
AY514751
DOGPHL
BCOGPHL
BCOGPHLAM
AY514751
DOGPHLAM
AY514751
DOGPHLAM
AY514751
DOGPHLAM
CPPHLAM
CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene,
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AC099716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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exon 2. DNA

linear

MAM 27-APR-1993

AR121629 Sequence AL031736 Human DNA AC116417 Mus muscu AC145916 Gallus ga CQ719769 Sequence

Sequence Sequence

AX894936 Sequence
BD030469 Sequence
AP177764 Homo Bapi
CQ718671 Sequence
MG3603 Human phosp
BC005269 Homo Bapi
AL135536 Homo Bapi
AL135374 Homo Bapi
AL13536 Homo Bapi
AL135310 Logaris fam
M16012 Canis fam
M16012 Canis card
M15393 Dog cardiac
Y00399 Dog cardiac
Y00399 Dog phospho
AR121629 Sequence

e, cloning of the chromosome 6

human

Tada, M. and

protein

of,

sarcoplasmic

reticulum

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KEYWORDS
SOURCE
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                                                                                DEFINITION
ACCESSION
VERSION
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ORGANISM
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OCPHLAM
LOCUS
                                                                                                                                       RESULT 3
BD247907
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Best Local S
Matches 71
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Best Local S
Matches 71
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                                        BD247907

Method for screening comp

BD247907

BD247907.1 GI:33057677

JP 2002541859-A/9.

Sus sp.

Sus sp.
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1 (bases 1 to 2841)

Rujii,J., Lytton,J., Tada,M. and MacLennan,D.H.
Rabbit cardiac and slow-twitch muscle express the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O.cuniculus mRNA for Y00761
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phospholamban gene
FEBS Lett. 227 (1), 51-55 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phospholamban.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y00761.1 GI:1661
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71; Conservative
                                                                                                                                                                                                                                                                                                                        Similarity
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/product="phospholamban"
/protein_id="CAA68730.1"
/db_xref="GI:1662"
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/db_xref="taxon:9986"
                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GOA:P20006"
/db_xref="UniProt/Swiss-Prot:P20006"
/translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryctolagus cuniculus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 336
               Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                          159 bp
; compounds.
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phospholamban.
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Pred. No. 1.1e-05;
0; Mismatches 31;
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Pred. No. 1.
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                 Euteleostomi;
Sus.
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VERSION
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TITLE
JOURNAL
Query Match
Best Local Similarity
Matches 70; Conserv
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Best Local :
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OS Artificial Sequence
pN JP 2002541859-A/13
pD 10-DEC-2002
pF 14-APR-2000 JP 2000612503
pF 14-APR-2000 JP 2000612503
pF 15-APR-1999 GB 9908670.4,15-APR-1999 US 60
PT RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42,C12N15/09,C12Q1/02,C12N15/00
CC Description of Artificial Sequence:HUMANIZED PIC
Key Location/Qualifiers
PT source 1..159
PT source /organism='Artificial Sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 CTTAATATGCCTCTTGCTGATTTGCATCATCGTGATGCTTCT 155
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OS Sus sp. (pi
OS Sus sp. (pi
PN JP 20025418
PD 10-DEC-2002
PF 14-APR-2000
PR 15-APR-1999
O1-JUN-1999 GB
PI RICHARD ZWA
PC C1201/42,C1
CC Method for
FH Key
FT source
FT source
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Method for screening compounds
Patent: JP 2002541859-A 9 10-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 159)

Zwall, R., Groenen, J. and Bogaert, T.

Method for screening compounds

Patent: JP 2002541859-A 13 10-DEC-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           synthetic construct synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BD247911 159 bp Method for screening compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         other sequences; artificial sequences.
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TP 2002541859-A/9
10-DEC-2002
14-APR-2000 JP 2000612503
15-APR-1999 GB 9908670.4,15-APR-1999 US
UN-1999 GB 9912736.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus sp."
/mol_type="genomic DNA"
/db_xref="taxon:9826"
                                                                                                                                              /organism='Artificial
Location/Qualifiers
                                                                                 /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.6%;
                   37.6%;
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Pred. No. 3.1e-05;
0; Mismatches 32;
   Score 50.8; DB 6;
Pred. No. 3.1e-05;
); Mismatches 32;
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                                    Length 159;
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Maximum DB
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Perfect score:
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Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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  Beq
1
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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001bs:*
6: geneseqn2001bs:*
6: geneseqn2002bs:*
7: geneseqn2002bs:*
9: geneseqn2003bs:*
10: geneseqn2003bs:*
11: geneseqn2004as:*
11: geneseqn2004as:*
11: geneseqn2004as:*
13: geneseqn2004as:*
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 1.0
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Length
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Aac06724 Human sec
Ach16933 Human sed
Ab161825 Colon ade
Adh04087 Antipsori
Adp21384 Gene Puri
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Ach16738 Human adu
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Adb53082 Primary r
Adr97285 Human pho
Abn22344 Human ORF
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30.8	30.8	30.8	30.8	30.8		31.2	31.2	31.4	31.4	32.6		33.6	33.6		33.6	33.6	33.6	33.6	•	33.6	u.	35	35	35
22.8	22.8	22.8	22.8	22.8	22.8	23.1	23.1	23.3	23.3	÷			24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	24.9	25.9	25.9	25.9
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Aak28730 Human bon	Aba24770 Probe #32	Aba44562 Human bre	Aai34661 Probe #33	Aba55007 Human foe	Aai13308 Probe #32	Abk74380 Bacillus	Adq79072 Novel can	Aax24906 Mouse elo	Acn44341 Mouse mRN	Adc86554 Human GPC	Adq21778 Human sof	Aac77686 Human can	Aaz77530 Human ova	Acn38837 Tumour-as	Adr25399 Breast ca	Adf81412 Leukaemia	Abk83658 Human cDN	Adc37617 Human nuc	Adl62294 Human ova	Adp07907 Human RAD	Abq60653 Human col	Aal41031 DNA encod	Aac85836 Nucleotid	Aac75801 Human ORF

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RESULT 1
AAC64967
15-APR-1999;
15-APR-1999;
01-JUN-1999;
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                                                                                                                                                                                                                                    Pig phospholamban cDNA.
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                                                                                                                                                   14-APR-2000; 2000GB-00009363
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99US-0129596P.
99GB-00012736.
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                                                                                            Bogaert
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The present invention is concerned with methods of using C. elegans identify compounds which are capable of up- and down-regulating the activity of the sacro/endoplasmic reticulum calcium ATPase (SERCA). protein is involved in cell signalling, and elevated levels affect cellular processes such as contraction, secretion and cell cycling.

This The

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Identifying modulators of sarco/endoplasmic reticulum calcium ATPase, useful potentially for treating disorders of calcium homeostasis, e.g cardiac hypertrophy.

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WPI;

2000-658082/64.

Disclosure; Fig 11; 108pp; English.

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RESULT 2
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11-APR-2002
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13-MAR-2002;
08-APR-2002;
10-APR-2002;
10-APR-2002;
                                                                                                                                                                                          Mendrick
Elashoff
                                                         Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
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2002US-0373602P
2002US-0374139P
2002US-03781370P
2002US-0378653P
2002US-0378653P
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Claim 44; SEQ

ij

NO 3624; 874pp;

English

The invention relates to a method of phospholamban polymorphism assessment in an individual which comprises comparing the analysis of uncleotide fragment with a predetermined phospholamban nucleotide fragment sequence to determine whether the individual carries a phospholamban polymorphism. The methods and phospholamban polymorphism fragment are useful for determining if an individual is at risk for

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SEQ

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15pp;

English

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value.
                                                                                                                                              Phospholamban polymorphism assessment in individual, for determining for developing cardiovascular disease, by comparing analysis of the nucleotide fragment with a predetermined phospholamban nucleotide
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ilarity 68.0%;
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GenCore version (c) 1993 - 2005
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BF547322 UI-R-C2p-
AI322542 mh89b06.y
BE115006 UI-R-BJ1-
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BX922974 BX922974
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7 UI-R-CSO-

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8 UI-R-CMO-

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AGENCOURT	EST213218	UI-R-ABO-	UI-R-DKO-																		

REFERENCE AUTHORS ACCESSION VERSION KEYWORDS RESULT 1
BX669692
LOCUS
DEFINITION SOURCE ORGANISM ORIGIN FEATURES COMMENT TITLE source Bonnet, A., Tosser-Klopp, G., Benne, F., Caban Soares, M., Bonaldo, F. and Hatey, F. A pig Normalised Multi-Tissue cDNA Library Unpublished (2003) Contact: Tosser-Klopp G Genetique Animale Institut National de la Recherche Agronomic Chemin de Borde-Rouge - Auzeville BP27, 31: Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan cedex, FRANCE Tel: 33 (0) 5.61.28.51.14

Fax: 33 (0) 5.61.28.53.08

Email: tosser@tollouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this BX669692 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0028i.c.02 Sprim, mRNA sequence. plate: 00 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 381) Sus scrofa Sus scrofa (pig) BX669692.1 GI:37979481 0028 row: c /clone="scac0028i.c.02"
/tissue_type="mixed"
/tissue_type="mixed"
/clone_Tib="Sus Scrofa library (scac)"
/clone_Tib="Sus Scrofa library (scac)"
/clone_Tib="Sus Scrofa library tissues: adipose tissue,
/note="Vector: p773D-pac vector; tissues: heart,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo uretral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder" /organism="Sus scrofa" /mol_type="mRNA" /db_xref="taxon:9823" Locat ow: c column: ion/Qualifiers Benne, F., Cabau, C., Villeger, S., N Agronomique BP27, 31326 Euteleostomi; Sus. EST 07-MAY-2004

Query Match

37.6%;

Score 50.8;

DB 5;

Length 381;

Castanet-Tolosan

Euteleostomi;

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RESULT 2
BX922974
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  RESULT 3
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Plate: 0013 row: j column: 14.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 702)

Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S., Soares, M., Bonaldo, F. and Hatey, F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Institut National de la Recherche
Chemin de Borde-Rouge - Auzeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Pig Normalised Multi-Tissue cDNA Library Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="scan0013d.j.14"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/clone_lib="Sus Scrofa library (scan)"
/clone_tib="sus Scrofa library (scan)"
/clone_tibsues: adipose tissue, brain, kidney, liver,
/note="tissues: stain, brain, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo uretral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
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68.6%;
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0; Mismatches 32
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Pred. No. 0.00033;
0; Mismatches 32
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Institut National de la Recherche
Chemin de Borde-Rouge - Auzeville
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
                                                                                                                                                                                                                                                                        BX924154 Sus Scrofa library (scan) S scan0011d.f.23 Sprim, mRNA sequence.
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Sus scrofa
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BX674983 Sus Scrofa library (scac) Sus scrofa cDNA clone
scac0039i.h.23 Sprim, mRNA sequence.
BX674983
                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                           Sus scrofa
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
  Soares, M.,
                         Bonnet, A.,
                                                     1 (bases 1 to 740)
                                                                                                                                                                 Sus scrofa (pig)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX674983.1
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/clone="scac0039i.h.23"
/tissue_type="mixed"
/clone=Tib="Sus Scrofa library (scac)"
/clone=Type="mixed"

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Tosser-Klopp, G., Benne, Bonaldo, F. and Hatey, F.
                                                                                                                                                                                                                          GI:41141002
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                                                                                  Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
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Pred. No. 0.00033;
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                               Benne, F.,
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                                  Cabau, C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/BTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                       US-09-549-872B-9
US-09-513-990C-1079
US-09-913-990C-1079
US-09-949-016-13181
US-09-949-016-13181
US-09-949-016-13588
US-09-949-016-12426
US-09-949-016-12336
US-09-949-016-12336
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US-09-949-016-202802
US-09-188-930-28
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13, Appl
10799, A
1439, Ap
13181, A
26, Appl
3, Appli
3588, Appli
1172, Ap
15336, A
15336, Ap
1536, Appl
636, App
636, A
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US-09-549-872B-9
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28 28.8 21.3 879 4 US-09-489-039A-5041 29 28.6 21.2 601 4 US-09-949-016-200764 30 28.6 21.2 601 4 US-09-949-016-200764 31 28.6 21.2 46343 4 US-09-949-016-16824 32 28.6 21.2 152583 4 US-09-949-016-17396 33 28.6 21.2 152583 4 US-09-949-016-17391 35 28.6 21.2 152583 4 US-09-949-016-17391 36 28.6 21.2 152583 4 US-09-949-016-17391 37 28.4 21.0 1855 4 US-09-949-016-17391 38 28.4 21.0 1855 4 US-09-949-016-1929 39 28.2 20.9 568 4 US-09-949-016-15578 39 28.2 20.9 568 4 US-08-956-171E-999 41 28.2 20.9 568 4 US-08-956-171E-999 42 28.2 20.9 603 3 US-08-816-346-5 43 28.2 20.9 1851 4 US-09-335-411-5 44 28.2 20.9 20.7 3 US-09-349-016-3036 45 28.2 20.9 20.7 3 US-08-16-346-1
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601 4 601 4 152583 152583 152583 1664583 4 1664976 603 3 1603 3 2907 3
US-09-489-039A-5041 4 US-09-949-016-200644 4 US-09-949-016-200790 4 US-09-949-016-12086 4 US-09-949-016-17391 5 4 US-09-949-016-17391 6 4 US-09-949-016-17391 7 4 US-09-949-016-12391 7 4 US-09-949-016-12578 7 US-09-949-016-12578 8 US-09-949-016-12578 9 US-08-956-1718-999 9 US-08-956-1718-999 9 US-08-916-346-5 9 US-09-949-016-3036 9 US-09-949-016-3036 9 US-09-949-016-3036
US-09-489-039A-5041 US-09-949-016-200790 US-09-949-016-16824 US-09-949-016-17390 US-09-949-016-17391 US-09-949-016-17391 US-09-949-016-17391 US-09-949-016-1578 US-09-949-016-15578 US-09-949-016-15578 US-09-949-016-15578 US-09-949-016-15578 US-09-949-016-15578 US-09-949-016-15578 US-09-949-016-15578 US-09-949-016-15578 US-09-149-016-1036 US-09-149-016-1036 US-09-149-016-1036 US-09-149-016-1036 US-09-149-016-1036

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RESULT 2
US-09-549-872B-13
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
ITILE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PAtentin Ver. 2.0
SEQ ID NO 9
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9
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Best Local Similarity 68.0
Matches 70; Conservative
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Pred. No. 1.2e-07;
0; Mismatches 32;
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US-09-513-999C-10799
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                                                                                         RESULT 4
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; ORGANISM: Homo sapiens
US-09-513-999C-10799
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PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
               Sequence 1439, Application US/09949016 Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10799
                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local S
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CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT: VENTER, J. Craig et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Description of Artificial Sequence:HUWANIZED OTHER INFORMATION: PLB cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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67; Conserv
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Similarity 68.6%;
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                                                                                                                                                                                                                                                                                          Conservative
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65.7%;
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Pred. No. 8.4e-
0; Mismatches
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Pred. No. 1.2e-07;
0; Mismatches 32;
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ches 35; Indels
                                                                                                                                                                                                                                                                                                                            DB 4;
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US-09-949-016-13181
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US-09-949-016-13181
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1439
                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13181
LENGTH: 16062
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 67; Conserv
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-9-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
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les 67; Conserv
12721
                                                                                      12661 TGAAATGCCTCAACAAGCACGTCAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCAT 12720
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  CTTAATATGTCTCTTGCTGATCTGTATCATCGTGATGCTTCT
                        TCTCATCTGCCTCCTGCTGATTTGCATTATCGTCATGCTCCT 119
                                                                                                                            TGAGAGAAAGGCCTCAGGCCAGGCAGAACCTCCAGAATGCTTTCATTGCTTTTTTGTCTGAT 77
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65.7%;
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Pred. No. 4.2e-05;
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Pred. No. 1.5e-05;
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                                                                                                                                                                                                                  Length 16062;
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OF DETECTION
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RESULT 6 US-09-124-671-26 · sequence 26, Application US/09124671A

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Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                         Minimum DB
Maximum DB
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seq length: 2000000000
                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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135
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                                                                                                                                                                                                                              Published Applications NA:*
L: /cgn2_6/ptodata/1/pubpna/US07
2: /cgn2_6/ptodata/1/pubpna/PCT_
gagagaaagcttatgcatga.....tcctgctcgaggagagagag 135
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

76	51	c 4	ω.	ი 2	ب	Result No.
50.8 46	50.8	108	108	135	135	Score
37.6 34.1	37.6	80.0	80.0	100.0	100.0	Query Match Length DB ID
159 159	159	108	108	135	-	ength I
15 19	15				20	BB
US-10-371-101-13 US-10-691-412-1	US-10-371-101-9	US-10-724-532-4	US-10-724-532-3	US-10-724-532-6	US-10-724-532-5	ID
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e 40, A e 78016 e 43089	, O	Sequence 3, Appli Sequence 7, Appli	e 1007, e 25701	രേഗ	Sequence 1260, Ap	. N F	000	جي ر	ต ผผ	Sequence 1076, Ap Sequence 5, Appli	e 1076,	e 3842, A	Sequence 26, Appl Sequence 26, Appl	26,	e 4217, A	e 5235,	e 3950,	e 162,	162	Sequence 4045, Ap

ALIGNMENTS

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US-10-724-532-5
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic TITLE OF INVENTION: Reticulum FILE REFERENCE: SR RPA CURRENT APPLICATION NUMBER: US/10/724,532 CURRENT FILING DATE: 2003-11-29 PRIOR APPLICATION NUMBER: US 60/430322 PRIOR APPLICATION NUMBER: US 60/430322 PRIOR FILING DATE: 2002-12-02 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin version 3.2 SEQ ID NO 5 LENGTH: 135 LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/10724532
Publication No. US20040203027A1
GENERAL INFORMATION:
APPLICANT: Reed, Thomas D
                                                                                                                                                    Query Match 100.0%; Score 135; DB 20; Best Local Similarity 100.0%; Pred. No. 7.7e-36; Matches 135; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: mus musculus
  61 ATTGCTTTTTGTCTGATTCTCATCTGCCTCCTGCTGATTTTGCATTATCGTCATGCTCCTG 120
                                                                                 1 GAGAGAAAGCTTATGCATGAGAGAAGGCCTCAGGCCAGAACCTCCAGAATGCTTTC 60
                                                      GAGAGAAAGCTTATGCATGAGAGAAGGCCTCAGGCCAGGCAGAACCTCCAGAATGCTTTC
                                                                                                                                                         Indels
                                                                                                                                                                                                     Length 135;
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FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 135
TYPE: DNA
ORGANISM: mus musculus
US-10-724-532-6
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                                                                                                                                       ; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-3
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US-10-724-532-3
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US-10-724-532-6/c
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APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
NUMBER OF SEQ ID NOS: 6
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APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.2 SEQ ID NO 3
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Publication No. US20040203027A1
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Publication No. US20040203027A1
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Best Local Similarity
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13 ATGCATGAGAGAGGCCTCAGGCCAGGCAGAACCTCCAGAATGCTTTCATTGCTTTTTGT 72
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                                                          80.0%; Score 108; DB 20; ilarity 100.0%; Pred. No. 1.1e-26; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
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Query Match
Best Local Similarity
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; ORGANISM: Sus sp.
US-10-371-101-9
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                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR TILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR FILING DATE: 2000-04-14
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Publication No. US20040203027A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/10371101 Publication No. US20030149995A1 GENERAL INFORMATION:
                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 9
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CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
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TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035.US
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 108
TYPE: DNA
ORGANISM: mus musculus
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                                    37.6%;
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                                  Score 50.8; DB 15;
Pred. No. 4.2e-07;
                      Mismatches
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7: gb p
9: gb
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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  38.8 2841
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37.6 159
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37.6 139
37.2 159
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Copyright (c) 1993 - 2005 Compugen Ltd.
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45	44	3	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
35	35	35.2	35.6	36.2	44.2	44.4	44.4	44.4	44.4	46	46	46	46	46	46	46	46	46	46	46	46	46.6	46.6	47	47
25.9	25.9	26.1	6.4	26.8	Ν	N	32.9	N	32.9	34.1	34.1	34.1	34.1	34.1	34.1	34.1	34.1	34.1	34.1	34.1	34.1	34.5	34.5	34.8	34.8
6481	5702	209299	184450	147419	315	2614	832	832	314	150290	66092	60797	1691	1635	1635	1635	980	480	480	323	306	3423	3312	177018	79895
ტ	σ	ຫ	N	9	σ	4	4	4	4	9	N	N	9	9	σ	σ	9	σ	σ	9	9	ű	ഗ	N	N
AR339585	CQ719769	AC145916	AC116417	HS738P11	AR121629	CFPHLX	DOGPLBA	DOGPHL	AY514751	HS509L4	AL136974	AL355356	BC005269	HUMPHLAM	AX329653	CQ718671	HSPLBG2	BD030469	AX894936	HUMPLAM	CQ447405	CHKPLB2	CHKPLB	AC099716	AC100317
AR339585 Sequence	CQ719769 Sequence	AC145916 Gallus ga	AC116417 Mus muscu	AL031736 Human DNA	AR121629 Sequence	Y00399 Dog phospho	M35393 Dog cardiac	M16012 Canine card	AY514751 Canis fam	Z99496 Human DNA s	AL136974 Homo sapi	AL355356 Homo sapi	вС005269 Ното варі	M63603 Human phosp	AX329653 Sequence	CQ718671 Sequence	AF177764 Homo sapi	BD030469 Sequence	AX894936 Sequence	M60411 Human phosp	CQ447405 Sequence	M59038 Chicken pho	M59039 Chicken car	AC099716 Mus muscu	AC100317 Mus muscu

ORIGIN	CDS	exon	mRNA	source	FEATURES	COMMENT	JOURNAL	TITLE	AULHORS	REFERENCE		ORGANISM	SOURCE	SEGMENT	VERSION	ACCESSION	DEFINITION	LOCUS	RABPHIAM2/C
Ca-ATPase" Ca-ATPase" Codon start=1 /product="phospholamban" /protein id="AAA31445.1" /db_xref="GI:165639" /translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINFCLILICLLL ICIIVMLL"		/product="phospholamban" 428 . 858	/organism="oryccolagus cuniculus" /mol_type="genomic DNA" /db_xref="taxon:9986" /tissue lib="rabbit genomic" join(M63600.1:855943,428858)	1	n/Qualifiers			he rabbit phospholamban gnment of the gene to h	MacLennan, D.H.	robert b willard H F	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	Oryctolagus cuniculus	Oryctolagus cuniculus (rabbit)	phospholamban. 2 of 3	M63601.1 GI:165636		ospholamban gene, partial exon 2.	RABPHLAM2 858 bp DNA linear MAM 27-APR-1993	

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RESULT 3
BD247907/c
LOCUS
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SOURCE
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Y00761
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 159)
                                                              Method for screening compb247907
BD247907.1 GI:33057677
JP 2002541859-A/9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Oryctolagus cuniculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eut
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
1 (bases 1 to 2841)
Esticia e Tutto
                                        Sus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phospholamban gene
FEBS Lett. 227 (1),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phospholamban.
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nilarity 69.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                /db_xref="GOA:P20006"
/db_xref="UniProt/Swiss-Prot:P20006"
/translation="MEKVQYLTRSAIRRASTIEMPQQARQNLQNLFINPCLILICLLL
ICIIVMLL"
                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="phospholamban"
/protein_id="CAA68730.1"
/db_xref="GI:1662"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryctolagus
/mol_type="mRNA"
/db_xref="taxon:9986"
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Pred. No. 1.3e-05;
0; Mismatches 31;
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Pred. No. 1.1e-05;
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AUTHORS
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Query Match
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Matches 70; Conser
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Matches 70
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TITLE
                                                                                                                                                                                     DEWGEN NV
OS Artificial Sequence
PN JP 2002541859-A 13 10-DEC-2002;
DEWGEN NV
OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2006612503
PR 15-APR-1999 GB 9908670.4,15-APR-1999 US 60
PR 15-APR-1999 GB 9912736.7
PI 17-APR-2000 JP 200612503
PR 16-APR-1999 GB 9912736.7
PI 17-APR-1999 GB 9908670.4,15-APR-1999 US 60
PI 17-APR-1999 GB 9912736.7
PI 17-APR-1999 GB 99127
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PN JP 2002541859-A/9

PN JP 2002541859-A/9

PD 10-DEC-2002

PF 14-APR-2000 JP 2000612503

PR 15-APR-1999 GB 9908670.4,15-APR-1999 US

POL-UUN-1999 GB 9912736.7

PI RICHARD ZWAAL, JOSG GROENEN, THIERRY BOGAERT

PC C1201/42,C12N15/09,C1201/02,C12N15/00

CC Method for screening compounds

FH Key Location/Qualifiers

FT source 1. 159

FT source /organism='Sus sp. (pig)'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155
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synthetic construct
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Method for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for screening compour Patent: JP 2002541859-A 13
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Zwaal, R., Groenen, J. and Bogaert, T.
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Location/Qualifiers
                                                                                                                                              /organism='Artificial
/organism="synthetic construct"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sus sp."
/mol_type="genomic DNA"
/db_xref="taxon:9826"
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Pred. No. 3.1e-05;
); Mismatches 32;
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Conservative

0

Score 50.8; DB 6; Pred. No. 3.1e-05; 0; Mismatches 32

DB 6;

Length 159;

Gaps

0

37.6%; 68.6%;

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No.
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Maximum DB
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1: geneseqn1900s:*
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Match
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135
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Listing first 45 summaries
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 ctctctctcctcgagcagga.....tcatgcataagctttctctc
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3117.004 Million cell upda
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  2959870667 residues
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Aac64967 Pig phosp
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Abn22344 Human ORF
Aac067724 Human oRF
Aac067724 Human adu
Ab161825 Colon ade
Adn94087 Antipsori
Adp21384 Gene PLN
Ach16738 Human adu
Ach17005 Human adu
Ach18023 Human adu
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444	446121	3 12	21316	10 25 66 5 3
AAI34661 ABA44562 ABA24770 AAK28730	ACN44341 AAX24906 ADQ79072 ABK74380 AAI13308 AAI13308 ABA55007	AAC77686 ADQ21778 ADC86554	ABK83658 ADF81412 ADR25399 ACN38837 AAZ77530	AAC75801 AAC85336 AAL41031 ABQ60653 ADP07907 ADL62294 ADC37617
Aa134661 Probe #33 Aba44562 Human bre Aba24770 Probe #32 Aak28730 Human bon	Mouse Novel Bacill Probe Human	Human Human Human	Abk83658 Human cDN Adf81412 Leukaemia Adr25399 Breast ca Acn38837 Tumour-as Aaz77530 Human ova	Aac75801 Human ORF Aac85836 Nucleotid Aal41031 DNA encod Abg60653 Human col Adg07907 Human RAD Adl62294 Human ova Adc37617 Human nuc

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ID AAGG49
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XX Pig; B
KW Cardia
KW Brody8
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15-APR-1999;
01-JUN-1999;
The present invention is concerned with methods of using C. elegans identify compounds which are capable of up- and down-regulating the activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). protein is involved in cell signalling, and elevated levels affect cellular processes such as contraction, secretion and cell cycling.
                                                                                                                                                                                                                                                                                             Identifying modulators of sarco/endoplasmic reticulum calcium ATR: useful potentially for treating disorders of calcium homeostasis, cardiac hypertrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pig; sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling; cardiac hypertrophy; heart failure; hypertension; Darier-White disease; Brodys disease; diabetes; ss.
                                                                                                                                                                                                                             Disclosure; Fig 11; 108pp; English.
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99GB-00012736.
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11-APR-2002
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11-APR-2002
19-APR-2002
22-APR-2002
08-MAY-2002
09-MAY-2002
09-MAY-2002
09-MAY-2002
                            Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene express; profile of a tissue or cell sample to a database of Tox mean and non-
                                                                                                Mendrick
Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxic effect; gene expression profile; hepatotoxicit toxicity marker; toxicity progression; drug screenin primary rat hepatocyte toxicity modelling; gene; ds.
                                                                          WPI;
                                                                                                                                                                            09-JUL-2002;
                                                                                                                                                                                                                                                                                                            08-APR-2002;
10-APR-2002;
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13-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ods can be used to identify compounds for use in the treatment muscle pathologies, cardiac hypertrophy, heart failure,
                                                                          2003-731472/69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATAGGTTCTGAAGGTTTTGACGTGCTTGTTGAGGCATTTCA
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2002US-037024BP.
2002US-037024BP.
2002US-0371135P.
2002US-03711413P.
2002US-0371413P.
2002US-0373601P.
2002US-0373602P.
2002US-0378652P.
2002US-0378652P.
2002US-0378652P.
2002US-0378652P.
2002US-0378652P.
2002US-0378652P.
2002US-0378652P.
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2002US-0378652P.
2002US-0378665P.
2002US-0378665P.
2002US-0378665P.
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                                                                                                          Porter M,
                                                                                                                                                      2003US-0442900P
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                                                                                                                                INC
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68.6%;
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                                                                                                           Johnson
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Pred. No. 6
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                                                                                                          <u>,</u> 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 T; 0 U; 0 Other;
                              comprises comparing a gene expression to a database of Tox mean and non-Tox
                                                                                                         Higgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hepatotoxicity;
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Matches
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                                                                                                                 The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                              Sequence
                 Local
70;
                 Similarity
                                                                                  701
Conservative
                                                                                BP;
                                                                                  184
               37.2%;
68.0%;
                                                                                A; 178 C;
<u>.</u>.
                   Score 50.2;
Pred. No. 1
                                                                                141 G; 198 T; 0 U; 0 Other;
Mismatches
                     .7e-05
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  33
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  Indels
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0;
Gaps
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329
269
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                          GAAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA 118
                                                                                       CAGAAGCATCACAATGATGCATATCAGCAGCAGACATATCAAGATGAGACAGAAATTGAT 270
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AAAGAGGTTCTGGAGGTTCTGACGCGCTTGCTGGGGCATTTCA
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RESULT 3
ADR97285/c
                                                                                            US2004191802-A1
                                                                                                                                                                                      Human phospholamban polymorphism fragment
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22-OCT-2002;
                              22-OCT-2003; 2003US-00691412
                                                               30-SEP-2004.
                                                                                                                                                                                                                       16-DEC-2004
                                                                                                                                                         human; phospholamban; polymorphism; cardiovascular disease.
                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                   standard; DNA;
 2002US-0420295P
                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                     159
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Phospholamban polymorphism assessment in individual, for determining for developing cardiovascular disease, by comparing analysis of the nucleotide fragment with a predetermined phospholamban nucleotide 15; sequence SEQ ID NO 1; 15pp; English riek the

WPI; 2004-689841/67

Kranias

EG,

Haghighi

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(HAGH/) KRAN/)

HAGHIGHI K. KRANIAS E G.

The invention relates to a method of phospholamban polymorphism assessment in an individual which comprises comparing the analysis of t nucleotide fragment with a predetermined phospholamban nucleotide fragment sequence to determine whether the individual carries a phospholamban polymorphism. The methods and phospholamban polymorphism fragment are useful for determining if an individual is at risk for

Claim 44; SEQ ID

NO 3624; 874pp; English

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Result
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111
113
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REFERENCE AUTHORS SOURCE ORGANISM ORIGIN ACCESSION VERSION KEYWORDS RESULT 1 BX669692/c FEATURES DEFINITION TITLE source Chemin de Borde-Rouge - Au cedex, FRANCE Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 381)

Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S., Soares, M., Bonaldo, F. and Hatey, F. Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this BX669692 Sus Scrofa library (scac) S scac0028i.c.02 Sprim, mRNA sequence. Genetique Animale Institut National de la A Pig Normalised Multi-Tissue CDNA Library Unpublished (2003) Sus scrofa (pig) Sus scrofa Contact: Tosser-Klopp G BX669692.1 GI:37979481 BX669692 0028 row: c /clone="scac00281.c.02"
/tissue_type="mixed"
/clone_Tib="Sus Scrofa library (scac)"
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/note="Vector: p773D-pac vector; tissues: heart,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo uretral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder" /mol_type="mRNA" /db_xref="taxon:9823" organism="Sus scrofa" ocation/Qualifiers column: 2. Recherche Auzeville 381 bp Agronomique BP27, 31326 Castanet-Tolosan mRNA linear EST Sus scrofa cDNA clone EST 07-MAY-2004

Query Match

37.6%;

Score 50.8;

DB 5;

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Castanet-Tolosan

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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
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Chemin de Borde-Rouge - Auzeville
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                                                                                                                              AAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA 118
                                                                                                                                                                                                               AGGAGCATGACGATAATGCAAATCAGCAGGAGGAGATGAGAATCAGACAAAAAGCAATG 76
                                                                                                                                                                                 AGAAGCATCACGATGATGCAAATCAGCAAGAGGCATATTAAGATGAGACAGAAATTGATA
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/tissue_type="mixed"
/dev_stage="from embryos to adults"
/dev_stage="from embryos to saults"
/clone_lib="Sus Scrofa library (scan)"
/clone_lib-"Sus Scrofa library (scan)"
/clone_library (scan)"
/clone_lib
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/mol_type="mRNA"
/db_xref="taxon:9823"
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68.6%;
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institut National de la Recherche Agronomique Chemin de Borde-Rouge - Auzeville BP27, 31326 cedex, FRANCE Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08
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Soares,M., Bonaldo,F. and Hatey,F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
Contact: Tosser-Klopp G
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/clone="scac0039i.h.23"
/clone="scac0039i.h.23"
/tissue_type="mixed"
/clone_Tib="sus_Scrofa_library_(scac)"
/clone="vector: pT773D-pac_vector; tissues: adipose tissue, prain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary_gland, seminal_vesicle, small_intestine, uterus, adrenals, bulbo uretral_gland, cerebral_trunk, epididymis, female_gonad, gall-bladder, hippocampus, large_intestine, male_gonad, melanocytes, stomach, udder"
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                           Sequence 13, Appl Sequence 10799, A Sequence 10799, A Sequence 13181, A Sequence 26, Appl Sequence 26, Appl Sequence 1076, Appl Sequence 1172, App Sequence 1172, App Sequence 1172, App Sequence 15336, Appl Sequence 15362, App Sequence 1562, App Sequence 1562, App Sequence 17304, App Sequence 17304, App Sequence 17304, App Sequence 17301, App Sequence 18001, A Sequence 11601, App Sequence 202802, Sequence 203, App Sequence 28, Appl Sequence 
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28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.4	28.4	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.8
20.9	20.9	20.9	20.9	20.9	20.9	20.9	21.0	21.0	21.2	21.2	21.2	21.2	21.2	21.2	21.2		21.3
2907	2120	1851	603	603	568	568	162914	1855	1664976	1664976	152583	152583	152582	46343	109	109	879
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US-08-816-346-1	US-09-149-476-160	US-09-949-016-3036	US-09-335-411-5	US-08-816-346-5	US-08-781-986A-999	US-08-956-171E-999	US-09-949-016-15578	US-09-949-016-1929	US-09-692-570-1	US-08-916-421B-1	US-09-949-016-17391	US-09-949-016-17390	US-09-949-016-12086	US-09-949-016-16824	US-09-949-016-200790	US-09-949-016-200644	US-09-489-039A-5041
	Sequence 160, App	Sequence 3036, Ap	Sequence 5, Appli	Sequence 5, Appli	Sequence 999, App	Sequence 999, App	Sequence 15578, A	Sequence 1929, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 17391, A	Sequence 17390, A	Sequence 12086, A	Sequence 16824, A	Sequence 200790,	Sequence 200644,	Sequence 5041, Ap

ALIGNMENTS

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APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 80/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 80/129,596
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN PATENTIN PATENTIN SOFTWARE: PATENTIN PATENT PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENT PATENTIN PATENT PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENT 
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Sequence 13, Application US/09549872B
PATENT NO. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.6
Best Local Similarity 68.6
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Sus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 AGAAGCATCACGATGATGCAAATCAGCAAGAGGCATATTAAGATGAGACAGAAATTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 AAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA 118
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Pred. No. 1.2e-07;
0; Mismatches 32;
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Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10799
                    RESULT 4
US-09-949-016-1439/c
US-09-949-016-1439/c
REQUELT No. 6812339
RETERIT NO. 6812339
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US-09-513-999C-10799/c
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TITLE OF INVENTION: Expressed Sequence Tags and
Patent No. 6783961
GENERAL INFORMATION: APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
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LENGTH: 15
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PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. APPLICANT: Giordano, J.Y.
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                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Descript
OTHER INFORMATION: PLB cDNA
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                                                                                                                                                                                                                                                                                                        Match 34.1%;
Local Similarity 65.7%;
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                                                                                                                                               AATAGATTCTGTAGCTTTTGACGTGCTTGTTGAGGCATTTCA
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 Craig et al.
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Pred. No. 8.4e-
0; Mismatches
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Pred. No. 1.2e-07;
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                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13181
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TITLE OF INVENTION: POLYMORPHISMS; METHODS OF
FILE REFERENCE: CL001307
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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US-09-949-016-1439
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13181
LENGTH: 16062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local Similarity
Matches 67; Conserv
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
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                                                                                                                                                                 Local Similarity nes 67; Conserv
12702
                                                                                    12762
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AATAGATTCTGTAGCTTTTGACGTGCTTGTTGAGGCATTTCA
                                       AAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCA
                                                                                    AGAAGCATCACGATGATACAGATCAGCAAGAGACATATTAAGATGAGACAGAAATTGATA 12703
                                                                                                                           AGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAATCAGACAAAAAGCAATG
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Pred. No. 4.2e-05;
0; Mismatches 35;
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Pred. No. 1.5e-05;
0; Mismatches 35
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OF DETECTION AND USES THEREOF
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RESULT 6 US-09-124-671-26/c ; Sequence 26, Application US/09124671A

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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135
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/ cgn2_6/ptodata/1/pubpna/VSOO_NSM_FOB.seq:*
/ cgn2_6/ptodata/1/pubpna/VSOO_NSM_FUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
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/ cgn2_6/ptodata/1/pubpna/USOO_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USIOA_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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6/ptodata/1/pubpna/US11A FUBCOMB.seq:*
6/ptodata/1/pubpna/US11 NEW PUB.seq:*
6/ptodata/1/pubpna/US60 NEW PUB.seq:*
6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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2603.465 Million cell updates/sec
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159						135	ength
19		15	20	20	20		BB
US-10-691-412-1	115-10-371-101-13	US-10-371-101-9	US-10-724-532-4	US-10-724-532-3	US-10-724-532-6	US-10-724-532-5	DB ID
Sequence 1, Appli	Semience 13 A	Seguence 9, Ap	Sequence 4, Ap	Sequence 3, Ap	Sequence 6, Ap	Sequence 5, Ap	Description
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US-10-369-493-43089	US-10-437-963-78016	US-10-470-048B-40	61-323	US-09-974-300-1671	-437-963-88	92-7	US-09-994-485-3	US-10-087-192-740	US-10-767-701-25701	US-10-292-798-1007	US-10-723-860-4598	US-09-925-301-80	-10-848-	342-887-	US-10-172-118-1260	-09-814-353-	US-10-425-115-167740	-10-425-114-	-10-723-518-	-09-969-034-	US-10-690-276-3	-10-023-219	09-727-384-5	-10-117-722	-10-	-09-918-995-1	-09-		-10-877-930-2	-10-815-514-2	US-09-918-995-5377	US-09-918-995-4217	US-09-918-995-5235	US-09-918-995-3950	US-10-843-641A-162	US-09-873-367C-162	
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TYPE: DNA
ORGANISM: mus musculus
US-10-724-532-5
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US-10-724-532-5/c
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CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10724532
Publication No. US20040203027A1
GENERAL INFORMATION:
                                                                                                                               Query Match 100.0%; Score 135; DB 20; Best Local Similarity 100.0%; Pred. No. 7.7e-36; Matches 135; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic TITLE OF INVENTION: Reticulum FILE REFERENCE: SR RPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed,
                                            135 CTCTCTCTCGAGCAGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAAT
61 CAGACAAAAAGCAATGAAAGCATTCTGGAGGTTCTGCCTGGCCTGAGGCCTTCTCTCATG 120
                                                                    1 CTCTCTCCTCGAGCAGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAAT 60
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                                                                                                                                      Indels
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FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 6
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TYPE: DNA
ORGANISM: mus musculus
US-10-724-532-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10724532 Publication No. US20040203027A1 GENERAL INFORMATION:
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APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10724532
Publication No. US20040203027A1
                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                          SEQ ID NO 3
                                                             Matches
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Best Local Similarity
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CURRENT FILLING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR FILING DATE: 2002-12-02
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, Thomas D
TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.2
                                                                                                                                                          LENGTH: 108
TYPE: DNA
ORGANISM: mus musculus
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16 CAGGAGCATGACGATAATGCAAATCAGCAGGAGGCAGATGAGAATCAGACAAAAAGCAAT
                                                             108;
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                                                         80.0%; Score 108; DB 20; ilarity 100.0%; Pred. No. 1.1e-26; Conservative 0; Mismatches 0;
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; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus s
US-10-371-101-9
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CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR APPLICATION NUMBER: 09912736.7
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR APPLICATION NUMBER: 09/549,872
PRIOR APPLICATION NUMBER: 09/549,872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/10371101 Publication No. US20030149995A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Publication No. US20040203027A1
                                                                                                                                                                       PRIOR FILING DATE: 2000-0
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 9
  Best Local Similarity Matches 70; Conserv
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                                        Query Match
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TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
TITLE OF INVENTION: Reticulum
FILE REFERENCE: SR RPA
CURRENT APPLICATION NUMBER: US/10/724,532
CURRENT FILING DATE: 2003-11-29
PRIOR APPLICATION NUMBER: US 60/430322
PRIOR PILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590,70035.US
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TYPE: DNA
ORGANISM: mus musculus
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37.6%;
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Conservative
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100.0%; Pred. No. 1.1e-26;
ative 0; Mismatches 0;
  Score 50.8; DB 1
Pred. No. 4.2e-07
0; Mismatches 3
                                            DB 15;
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